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Selection for high β -glucan content in oat grain

by

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For the Major Program

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For the Graduate College

This dissertation is dedicated to my mother, Gloria Martinez, who has always been there.

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ABSTRACT

High serum cholesterol level is a major risk factor of premature heart disease in humans. Oat (*A. sativa* L.) β -glucan lowers serum cholesterol in humans when is consumed in the daily diet. Development of oat cultivars with greater groat β -glucan content would increase the nutritional and economical value of the crop. The first objective of this study was to determine the progress from phenotypic selection of individual S_0 plants for high β -glucan content in two oat (*Avena sativa* L.) populations. The second objective was to determine the predominant gene action for β -glucan content and to estimate changes in genetic variances and broad sense heritability in those populations. The third objective was to estimate the correlated response of unselected agronomic and grain quality traits and genetic covariances and correlations between these traits and β -glucan content in the same populations.

The initial (C0) and selected (C1) generations of two genetically broad-based oat populations, IABG1 and IABG2, were evaluated in a field experiment in 1996 and 1997 at two Iowa locations. Mean β -glucan content increased 5.9 g kg^{-1} and 2.6 g kg^{-1} , and the genetic variance decreased 9.3% and 21.8 %, following selection in IABG1 and IABG2. Heritability estimates ranged from 0.49 to 0.65 on a sample-basis and from 0.80 to 0.88 on a line-mean basis. Additive variance was the only substantial component of genetic variance. Genotype-by-environment interaction was significant. However, ranking of $S_{0:1}$ lines for β -glucan content across environments was generally consistent, with correlations of genotypic β -glucan contents ranging from 0.63 to 0.82 across pairs of environments. Some experimental lines had significantly greater β -glucan content than the best checks.

Phenotypic selection for high groat β -glucan content will be effective to develop cultivars with elevated levels of β -glucan.

Mean yield, biomass, and test weight were significantly reduced by 19, 17, and 2%, respectively, in IABG2, and were not affected in IABG1. Mean protein content significantly increased by 4.9% in IABG1, whereas the mean oil content and heading date did not change in any population. Plant height significantly decreased by 3% in IABG1. The genotypic variance of all traits was not affected, except for that of plant height, which increased in IABG2. Selection increased negative genetic correlations of β -glucan content with yield, biomass, and oil content in both populations, and with heading date and height in one population. Selection for high β -glucan yield (the product of β -glucan content and grain yield) was proposed to improve β -glucan content and grain yield simultaneously.

CHAPTER 1. INTRODUCTION

High levels of blood cholesterol in humans are strongly associated with coronary heart disease (Mayes, 1990; Shekelle et al., 1981). Oat soluble fiber, when added to the daily diet, lowers serum cholesterol (Kurtzweil, 1996). This lowering effect tends to be greater in individuals with initially high blood cholesterol levels (Ripsin et al., 1992). The (1→3),(1→4)- β -D-glucan, also referred as β -glucan, has been identified as the active component of the soluble fiber responsible for lowering blood cholesterol (Davidson et al., 1991; Klopfenstein and Hosenev, 1987). β -glucan is a cell wall polysaccharide found in the endosperm and subaleurone layer of seed of Gramineae. Among cereals, oat and barley have the highest concentrations of β -glucan. However, oat has a larger proportion of soluble β -glucan (Lee et al., 1997). The development of oat cultivars with greater β -glucan is an alternative to increase the nutritional and economic value of the crop.

Oat β -glucan is a polygenic trait with intermediate heritability when measured on a single-plant basis. Some evidence indicates that β -glucan is under the control of genes with mainly additive effects and no interallelic interaction (Kibite and Edney, 1998; Holthaus et al., 1996). Although genotype-by-environment interaction for β -glucan content sometimes is a significant source of variation, the ranking of genotypes is generally consistent across environments (Lim et al., 1992; Peterson, 1991). The characteristics of the inheritance of β -glucan and the recent technology developed to measure the trait suggest that oat β -glucan content could be effectively increased through a selection program.

Research Objectives

The first objective of this study was to determine the progress from phenotypic selection of individual S_0 plants for greater β -glucan content in two oat populations. The second objective was to determine the predominant source of genetic variance for β -glucan content and to estimate changes in genetic variances and broad sense heritability in those populations. The third objective was to estimate the correlated response of unselected traits and genetic covariances and correlations among traits in the same populations. The results of this study will provide valuable information to support the development of new oat cultivars with greater β -glucan concentrations.

Dissertation Organization

This dissertation consists of an Abstract, an Introduction, a Literature Review, two manuscripts, Conclusions, four Appendices, and References cited in the Introduction, Literature Review and Appendices. The first manuscript describes the procedure used to develop two genetically broad-based oat populations, and the selection method for greater β -glucan content, and the genetic progress from selection. The second manuscript discusses the correlated response to selection for greater β -glucan content in the two populations, with emphasis on the changes of means, genetic variances, heritabilities, and genetic correlations of unselected agronomic and grain quality traits.

CHAPTER 2. LITERATURE REVIEW

Oat is sixth among cereal crops in world production after wheat (*Triticum aestivum* L.), maize (*Zea mays* L.), rice (*Oryza sativa* L.), barley (*Hordeum vulgare* L.) and sorghum [*Sorghum bicolor* (L.) Moench] (Hoffman, 1995). Russia is the largest oat producer. Canada and Australia are the major exporters (USDA, 1999). In the United States, oat ranks sixth in cultivated area after maize, wheat, soybean (*Glycine max* L.), sorghum, and barley. The national average yield was 2166 kg ha⁻¹ in 1998 (USDA, 1999). In Iowa, oat is the major small grain crop, and it is used for production of grain and straw, as a companion crop, and as forage. In 1998 in Iowa, 85,050 hectares of oat were harvested for grain with an average yield of 1865 kg ha⁻¹ (Holland and Skrdla, 1998).

Oat breeding programs in the U.S. concentrated their efforts from the 1900's to the 1960's on increasing resistance to crown rust disease (*Puccinia coronata* Corda.) and to improving agronomic traits such as lodging resistance and test weight (Browning et al., 1964). Pure line selection from germplasm introduced from Europe was the primary breeding method until the 1930's, when selection following hybridization became more common (Frey, 1985; Simons, 1970). Since the 1960's, new sources of parental germplasm were introduced and selection was conducted for yield *per se* (Rodgers et al., 1983). The grain yield improvement achieved with the release of improved oat cultivars over time has been estimated in several experiments. Wych and Stuthman (1983) evaluated nine cultivars released in Minnesota from 1923 to 1979. They reported an average annual rate of increase of 0.8 % for grain yield. They observed that lodging has been reduced, kernel weight has

been increased, and the number of kernels per unit area has decreased over time. Langer et al. (1978) estimated that grain yield increased by 0.22 % per year from 1932 to 1973 through the release of 60 cultivars. They suggested that the low rate of yield gain might be the result of the limited genetic variability for grain yield contained in the germplasm introduced from northern Europe to the midwestern U.S. Rodgers et al. (1983) reported an increase of 0.47 % per year in grain yield of midseason-maturity cultivars released from 1941 to 1975 and a 3.2 % increase per year in the grain yield of midseason cultivars released from 1975 to 1980. They attributed the larger rate of increase in yield from 1975 to 1980 to both selection for yield *per se* and the introduction of new parental germplasm. Lynch and Frey (1993), after studying nine cultivars and one experimental line released from 1914 to 1987, concluded that oat breeding has improved the performance of oat cultivars in stress environments.

To increase the economic value of the oat crop and make it more competitive, plant breeders have selected for altered chemical composition of the grain (Holland, 1997; Welch, 1995; Welch, 1985). Whole oat grain consists of a nutritious groat (caryopsis) covered by a non-nutritious hull that is primarily insoluble fiber (Wood, 1993). Dehulling is the first step in processing oat grain for food. Therefore, breeding for improved grain chemical composition in oat has been focused on the chemical properties of groats. Even before selection for improving grain chemical composition, oat was one of the most nutritious cereals. Oat grain protein has a well-balanced amino acid composition and greater digestibility than legume proteins (Barnes, 1982). The oil content of oat is greater than other cereals. Approximately 40% of oat oil fatty acids are polyunsaturated (Welch, 1985; Barnes, 1982). Evaluation of sources of variability for protein and oil contents, studies of their

inheritance, and establishment of selection programs to improve them have resulted in the development of oat lines with greater oil content, and lines and cultivars with greater protein contents (Schipper and Frey, 1992; Schipper et al., 1991; Schipper and Frey, 1991; Forsberg and Shands, 1989; Saastamoinen et al., 1989a; Kuenzel and Frey, 1985; Thro et al., 1985; Frey, 1975; Lyrene and Shands, 1975; Baker and Mckenzie, 1972).

Recently, the effect of oat soluble fiber on lowering serum cholesterol in humans has renewed interest in breeding for altered chemical composition of oat grain (Sacks, 1991). Demand for oat cultivars with greater soluble fiber content is expected (Stuthman, 1995).

Effect of Oat Soluble Fiber on Serum Cholesterol in Humans

Levels of serum cholesterol are strongly related to coronary heart disease risk (Mayes, 1990; Shekelle et al., 1981). The effect of diet on serum cholesterol is, therefore, a major concern in human nutrition. Individuals who base their diet on vegetable products tend to show lower levels of serum cholesterol (Kushi et al., 1985; Stamler, 1979). Sacks et al. (1975) reported that a group of 116 people who changed to a vegetarian diet for three years had much lower levels of serum cholesterol than the control population. Similarly, the risk of coronary heart disease among non-vegetarian Seven Day Adventists (SDA) was significantly greater than vegetarian SDA members after adjusting for other risk factors such as smoking, hypertension, heart disease, diabetes, and insufficient exercise (Phillips et al., 1978).

Most proposals to lower serum cholesterol involve a change in the diet. Consumption of saturated fatty acids and cholesterol in the diet increases the serum cholesterol levels. Conversely, increasing polyunsaturated fatty acids and decreasing cholesterol in the daily diet

may reduce serum cholesterol (Royce et al., 1984; Keys et al., 1965). This observation has led physicians to recommend reducing total intake of fat, saturated fatty acids, and cholesterol to lower serum cholesterol (Van Horn et al., 1991). However, a long-term diet that restricts many foods might not be acceptable to many people (Sacks, 1991). An alternative strategy is the inclusion of foods in the daily diet that lower serum cholesterol both directly and indirectly, by displacing foods containing fat and cholesterol. Dietary fibers, resist hydrolysis by gastrointestinal enzymes, and have been shown to reduce serum cholesterol levels in humans. Dietary fibers include lignin, cellulose, pectin, β -glucan, and some hemicelluloses (Theander et al., 1993; Shinnick et al., 1991). Khaw and Barnett-Connor (1987) examined the relationship between dietary fiber and heart disease mortality for a period of 12 years in a southern California population. They reported that each 6 g increase in daily fiber intake was associated with a 25 % reduction in heart disease mortality. Insoluble fibers like cellulose and wheat bran usually do not lower serum cholesterol (Behall et al., 1984; Jenkins et al., 1975), while soluble fibers like guar, pectin, and oat bran lower the blood cholesterol level (Shinnick et al., 1991; Van Horn et al., 1988; Jenkins et al., 1975). Denmark-Wahnefried et al. (1990) studied the effect of low fat, low cholesterol and oat bran supplementation diets on 71 hypercholesterolemic men and women for a four-week period. They found reductions in total serum cholesterol from the original levels from 10 to 17% with all diets and no significant differences among diets.

Among sources of dietary fiber, oat bran and oatmeal have been most intensively studied for their potential to reduce blood cholesterol (Sacks, 1991). Anderson et al. (1984) reported that a 21-day oat bran diet decreased serum cholesterol concentrations by 19% in 20

hypercholesterolemic men. Van Horn et al. (1988) found a serum cholesterol reduction of 10% in 236 people after consuming a diet recommended by the American Heart Association and additionally enriched with oatmeal.

There are two forms of serum cholesterol: plasma high-density lipoprotein cholesterol (HDL-C), and low-density lipoprotein cholesterol (LDL-C). These two forms need to be distinguished when describing the effects of oat on cholesterol levels because they have opposite effects on coronary heart disease. Greater levels of HDL-C are related to lower incidence of coronary heart disease, whereas greater levels of LDL-C are associated with greater levels of coronary heart disease (Castelli et al., 1986; Stamler, 1979; Miller et al., 1977). Oat soluble fiber lowers serum LDL-C levels and the risk of coronary heart disease (Anderson et al., 1984). Oat soluble fiber tends to be more effective in individuals with high initial serum cholesterol concentration (Shinnick et al., 1991). Van Horn et al. (1991) reported that an eight-week diet enriched with two servings per day of instant oats equivalent to 5.6 g of total dietary fiber per day, of which 2.2 g was soluble fiber, reduced serum total cholesterol by 0.4 mmol L⁻¹ and LDL-C by 0.25 mmol L⁻¹ of hypercholesterolemic adults. Anderson et al. (1990) found that a two-week diet supplemented with oat-bran cereal diet containing 3.5 g of soluble fiber reduced serum total cholesterol by 5.4 % and LDL-C by 8.5 % compared with a corn flakes-supplemented diet. Bartran et al. (1992) replaced the breakfast of 13 hypercholesterolemic individuals with oat bran cereal for three weeks. Total serum cholesterol and LDL-C were reduced by 8 to 11% compared with a three-week baseline period. Apolipoprotein B₁₀₀, (a major component of LDL-C), was decreased by 25%.

Swain et al. (1990) and Sacks (1991) questioned the direct efficacy of oat bran on lowering of serum cholesterol levels. They attributed the changes in serum cholesterol only to the effect of replacing dietary fat and cholesterol with oat bran. Shinnick et al. (1991), however, suggested that this result was an artifact of experimental conditions, and that oat bran does have a direct effect of lowering blood cholesterol. Welch (1995) summarized the findings of 37 studies from 1980 to 1993 that utilized oat bran to lower serum cholesterol. He found that 35 studies reported reductions in serum cholesterol, of which 22 were significant. Ripsin et al. (1992) performed a meta-analysis that summarized published and unpublished clinical trials that assess the effect of the addition of oat soluble fiber to the diet of free-living subjects on the blood cholesterol level. After analyzing the available data and removing the effects of potentially confounding variables, they concluded that there is strong evidence that supports the hypothesis that consumption of approximately 3 g per day of soluble fiber from oat products can lower the total cholesterol from 0.13 to 0.16 mmol L⁻¹, particularly in those individuals with initially high blood cholesterol levels. The U.S. Food and Drug Administration describes dietary fiber as a heart-healthy food and has recently claimed that it may help to lower serum cholesterol (Kurtzweil, 1996).

The (1→3),(1→4)- β -D-glucan (β -glucan) has been identified as the active component of the soluble fiber that lowers serum cholesterol in studies conducted in rats and humans (Davidson et al., 1991; Klopfenstein and Hosney, 1987). Tietzen et al. (1990) compared the effect of including regular oat bran, cellulose, and oat bran treated with β -D-glucanase to depolymerize the β -glucan to oligosaccharides, in diets of three groups of 10 male rats for 5 weeks. They found that the diet containing enzyme-treated oat bran produced the highest

serum and LDL cholesterol. This result suggests that the β -glucan fraction is responsible for lowering serum cholesterol. Behall et al. (1997) studied the effect of two diets containing oat fiber extracts with 1% and 10% β -glucan, on 23 mildly hypercholesterolemic individuals for a five weeks period in a crossover pattern. They found that total and LDL cholesterol levels decreased significantly with both diets and that the reduction in total cholesterol level was greater for the diet containing greater β -glucan content. Therefore, oat varieties with greater concentrations of β -glucan are desirable for their ability to lower blood cholesterol levels.

Various mechanisms for lowering cholesterol by oat fiber have been proposed. One potential mechanism is through an increase in bile acids or neutral steroids. Cholesterol is eliminated from the body by excretion of either bile acids or neutral steroids in the feces (Mayes, 1990). Soluble fibers have been associated with the increased excretion of bile acids and neutral steroids (Lia et al., 1995; Anderson and Chen, 1986). Kretsch et al. (1979) reported that a diet enriched with oat bran increased the fecal bile acids of 60 men. However, the serum cholesterol was not reduced. They suggested that the daily cholesterol intake might contribute to the lack of response in the total blood cholesterol of the 60 men. Judd and Truswell (1981) found a reduction of blood cholesterol and an increase of the fecal fat and bile acid excretion of 47% and 35%, after supplementing oatmeal to 10 subjects for 3 weeks.

Another mechanism by which oat bran may decrease cholesterol is via its effect on blood insulin levels. Frequent exposure of cell walls to insulin for long periods may contribute to the development of atherosclerotic lesions by increasing the cholesterogenic state (Flodin, 1986). Increased viscosity of soluble fibers reduces postprandial blood glucose

and insulin levels (O'Connor et al., 1981; Jenkins et al., 1975), which, in turn, may reduce cholesterol levels. Ellis et al. (1988) applied three different guar doses and a control in the diet of 8 non-diabetic individuals. They did not find any effect on blood glucose, but they found a reduction of the insulin level.

In contrast to its positive effect in human nutrition, β -glucan has an undesirable effect in animal feed since it is associated with reducing feed efficiency and growth in young chicks and swine (Cave et al., 1990). β -glucan apparently reduces the metabolizable energy for animal feed (Cave et al., 1989). Growth and feed conversion of chicks and swine fed with oat groats may be improved when their diet is supplemented with β -glucanase (Edney et al., 1989; Hesselman et al., 1982). Breeding for lower β -glucan content in feed oats is preferable because this would decrease input costs and increase the profitability of animal production (Kibite and Edney, 1998).

Structure and Properties of β -Glucan

Mixed-linkage (1 \rightarrow 3),(1 \rightarrow 4)- β -D-glucan, referred to as β -glucan, is a component of the cell wall in seeds of the Gramineae (Stinard and Nevins, 1980; Nevins et al., 1978). In oat and barley grains, β -glucan is found mainly in the cell wall of the endosperm and the subaleurone layer (Wood et al., 1983; Nevins et al., 1977). β -Glucan is a linear, unbranched polysaccharide composed of approximately 70% 4-0-linked β -D-glucopyranosyl units and 30 % 3-0-linked β -D-glucopyranosyl units (Parrish et al., 1960; Aspinall and Carpenter, 1984) organized mainly in two types of structural sequences. In the first type of sequence, a single β -(1 \rightarrow 3) linkage alternates with two β -(1 \rightarrow 4) linkages and in the second type a single β -

(1→3) linkage alternates with three β -(1→4) linkages (Parrish et al., 1960). β -glucan may be considered structurally as a chain of (1→3)-linked cellotriosyl and cellotetraosyl units (Parrish et al., 1960; Wood et al., 1991) in an approximate ratio of 2:1 for oat β -glucan and 3:1 for barley and rye β -glucan (Wood et al., 1994). The arrangement of these units in the polysaccharide is not known.

In general, solubility and viscosity of a substance are controlled by its structure and molecular weight. Differences of the physical properties in cereal β -glucan are related to structure rather than molecular weight (Wood, 1994). Woodward et al. (1983) reported that approximately 90% of the β -glucan polysaccharide consists of cellotriosyl and cellotetraosyl units separated by single (1→3)- β -linkages. The remaining structure contains blocks of four to 15 (1→4) linkages. There is controversy about the presence of consecutive (1→3) linkages in oat β -glucan (Wood et al., 1994). Woodward et al. (1983) proposed that the differences in solubility of cereal β -glucans may be explained by differences in the amount of adjacent (1→4) linkages.

Total mixed-linked (1→3),(1→4)- β -D-glucan can be classified as either water-soluble or water-insoluble β -glucan (Theander et al., 1993; MacArthur-Grant, 1986). Solubility refers to the component of β -glucan extractable with water from the total β -glucan (Wood, 1993; Åman et al., 1989). Solubility is influenced by several factors, such as structure, interrelations between cell-wall constituents, pretreatment, extraction variables, and the activity of endogenous enzymes (Wood, 1993). Åman et al. (1989) reported that 90% of the mixed-linked β -glucan extracted with water at 38 °C from oat grain was soluble before harvest, whereas 85% was soluble at harvest and during storage. These proportions vary with

different combinations of sources of β -glucan and extraction conditions (Pretince et al., 1980; Wood et al., 1991c).

Water-soluble mixed-linkage β -glucan has the ability to form highly viscous solutions (Theander et al., 1993). Viscosity is considered to have an important role in the ability of oat bran to lower serum cholesterol (Wood, 1993). Wood et al. (1989) compared oat gum prepared in a pilot plant with oat gum prepared in a laboratory, both of which consisted of approximately 80% β -glucan. They found that the oat gum prepared in the laboratory showed 10 times more viscosity calculated at a shear rate of 1 sec^{-1} than the oat gum prepared in the pilot plant. This difference in viscosity between the two types was attributed to a change in molecular weight in the pilot-plant oat gum. Wood et al. (1991c) determined the oat gum molecular weight by size-exclusion chromatography using a high performance liquid chromatography gel column. They reported that the laboratory oat gum had almost twice the molecular weight of the pilot-plant oat gum. The molecular weight of β -glucan extracted from groats and bran from four commercial oat cultivars ranged from 2.89 to $3.14 \times 10^6 \text{ Da}$.

Methods to Measure β -Glucan Content

Among the several methods developed to measure the β -glucan content in agricultural products, the enzymatic and the fluorometric methods are the methods accepted as the standard procedures because they have been thoroughly laboratory tested and proven to be accurate and reliable (McCleary and Codd, 1991; Munck et al., 1989).

The enzymatic method can be applied to oat, barley, malt, and beer samples to determine (1 \rightarrow 3),(1 \rightarrow 4)- β -D-glucan concentration. The first step in this method consists of

grinding the grain samples and incubating them in buffer at 100 °C to increase the susceptibility of β -glucan to enzymatic hydrolysis. The sample is cooled to 40 °C and treated with lichenase, a highly purified (1 \rightarrow 3),(1 \rightarrow 4)- β -D-glucanase from *Bacillus subtilis*, to depolymerize the β -glucan to tri-, tetra- and greater-order oligosaccharides that later are hydrolyzed to glucose using purified β -D-glucosidase. The glucose content is determined using glucose oxidase/peroxidase reagent. This is considered an appropriate method for the routine analysis of β -glucan in samples derived from plant breeding programs (Cho and White, 1993; Munck et al., 1989; McClear and Glennie-Holmes, 1985).

The enzymatic method is specific for mixed-linkage β -glucan because the enzymes used are highly purified. Sometimes the β -glucanase preparations contain impurities of other enzymes that degrade other carbohydrates, such as starch, and the β -glucan content is overestimated (Jørgensen and Aastrup, 1988; Munck et al., 1989). Åman and Hesselman (1985) avoided this problem by degrading starch using a thermostable α -amylase and amyloglucosidase before degradation of β -glucan with lichenase. The commercial availability of lichenase and β -glucosidase in kit form has helped to make this method the most accepted assay for β -glucan (Wood, 1993).

The fluorometric method also can be applied to oat, barley, malt, and beer samples. This method is based on flow injection analysis (FIA) and fluorescence detection. The principle is that the fluorescence intensity of fluorochrome calcofluor in aqueous solution increases with the addition of soluble β -glucan (Munck et al., 1989). The first part of the fluorometric method consists of extracting the water soluble β -glucan. Solubilisation of the total β -glucan content is achieved by degradation using mild acid hydrolysis. Lim et al.

(1992) described the procedure used to analyze the β -glucan content in oat as follows. Groat samples are dried at 80 °C for 18 h and ground. The dry-basis sample weights are obtained for each sample. Then, each sample is placed in a screw cap test tube with a solution of water and α -amylase, sealed and heated with stirring in water at 100 °C for 1 h, and then cooled in water for 10 minutes. 0.075 M H_2SO_4 is added to the tubes. The tubes are heated with stirring for exactly ten minutes in water at 100 °C and cooled in water for 10 minutes. The samples are transferred to polypropylene tubes and centrifuged for 11 minutes. Three subsamples from each sample are transferred to cultured tubes and diluted with distilled water.

The system for measuring β -glucan using flow injection analysis (FIA) consists of a random sampler, injection module, fluorescence spectrophotometer, and a computer. Each sample is mixed with a carrier buffer (0.1M tris solution), conducted by the pump into the injection module where it is mixed with the fluorescence color reagent (0.005 % cellufluor solution), and carried from there to the fluorescence spectrophotometer to monitor the increase in fluorescence intensity, which is recorded by the computer. The maximum increase in intensity (peak area) is recorded. Standards with known amounts of β -glucan are used to calculate the β -glucan content. The peak area of each sample is converted to milligrams of β -glucan per liter using a regression equation obtained with calibration standards (Lim et al., 1992; Jørgensen, 1988).

The enzymatic and fluorometric methods have acceptable repeatability and reproducibility. The correlation between their measurements is greater than $r = 0.97$. However, the fluorometric method is more suitable when a large number of samples have to

be analyzed routinely because it is less laborious than the enzymatic method (Jørgensen, 1988; Munck et al., 1989).

The β -glucan content has been also estimated using indirect methods like near-infrared reflectance spectrometry (NIRS) analysis and acid extract viscosity. Although these methods are less accurate than the enzymatic method and flow injection analysis, they are faster and simpler to conduct (Aastrup, 1979; Jørgensen and Aastrup, 1988).

NIRS analysis is a method widely used to measure the protein, moisture, oil, starch, sucrose, fiber, grain texture, and lysine contents of agricultural products (Osborne et al., 1983; Osborne, 1981). This method is based on the relationship between the reflectance of near-infrared light by substances and their chemical composition (Henry, 1985). Chemical bonds in molecules are always vibrating. The molecules absorb radiation when the vibration is at the same frequency of the radiation wave. Since vibrations occur at fixed frequencies, molecules have characteristic absorption bands corresponding to these fixed frequencies. In addition, the radiation absorbed is proportional to the number of similar chemical bonds that are vibrating (Osborne, 1981). The near-infrared region of the electromagnetic spectrum is located between the region visible to the human eye (400-700 nm) and the infra-red (IR) region (2500-15000 nm). Substances have absorption bands in the NIR and IR regions. While many constituents of agricultural products and food have strong absorption at the wavelengths in the infra-red region making the analysis very difficult, the NIR region is less complex to analyze because not all constituents absorb in bands of this region, but the absorption bands of protein, oil, and some other constituents are strong enough to measure (Osborne, 1981; Norris, 1964).

Constituents of food absorb differentially in several wavelengths. Overlapping of absorption bands occurs among constituents. Multiple wavelength readings on a sample allows measurement of several constituents simultaneously. For example, if three different constituents, protein, oil, and β -glucan, have absorption at the same six wave lengths but with different magnitudes, a multiple regression equation of the constituent content against the radiation absorption for each constituent can be obtained by estimating the constituent concentration with a very accurate chemical method (like FIA or the enzymatic method) and making absorption measurements with a NIR spectrophotometer. The regression equation is used to predict the constituents concentration of other samples based on their NIRS readings (Henry, 1985; Ben-Gera and Norris, 1968; Osborne, 1981). The NIRS method is useful for plant breeding for improved nutritional quality because it allows simultaneous rapid estimation of multiple nutritional components of many genotypes with good accuracy.

Another quick method to estimate the β -glucan content is based on the correlation of β -glucan content and viscosity of extracts of oats and barley. Most of the viscosity of malt extracts is due to β -glucan, and viscosity due to other components is generally constant among cultivars (Bendelow, 1975). Aastrup (1979) reported a correlation of 0.99 between viscosity of acid flour extract and acid-soluble β -glucan content in 18 genotypes of barley. Low correlation of viscosity with total β -glucan and no correlation with insoluble β -glucan were found. He estimated a linear regression equation of soluble β -glucan content against the natural logarithm of the acid extract viscosity and suggested that this method could be used to predict the soluble β -glucan content of other genotypes based on their acid extract viscosity.

Other authors found no correlation between soluble β -glucan content and viscosity (Anderson et al., 1978; Wainwright and Buckee, 1977). Aastrup (1979) attributed the inconsistency of the correlation between soluble β -glucan and viscosity to the wide diversity of methods used to extract β -glucan, given that the amount of β -glucan extracted is highly dependant on the extraction conditions. Bhatti (1992) extracted oat meal using a procedure similar to the one proposed by Aastrup (1979) and found correlations between acid extract viscosity and total β -glucan content of 43 and 27 % for two different sets of oat genotypes, respectively. He concluded that the viscosity of acid extracts was a poor indicator of total β -glucan. More recently, Luhadoo et al. (1998) reported correlations greater than 0.90 between both total and extractable β -glucan and viscosity of samples of 10 commercial oat brans ground and dispersed in phosphate buffer. Doehlert et al. (1997) found a correlation of 0.85 between viscosity and β -glucan content of flour slurries obtained by adding water at 25 °C to enzyme-inactivated groat flours of commercial oat cultivars. They suggested that this procedure would be a suitable method for screening β -glucan content in preliminary evaluations of breeding oat lines.

β -Glucan Concentrations

Oat and barley grains are the best sources of β -glucan among the commonly-grown cereals. Several studies demonstrated wide variation in the β -glucan concentration among different oat genotypes adapted to North America. Peterson (1991) analyzed the groat β -glucan contents of 12 commercial cultivars. He found that the β -glucan contents averaged across locations and years ranged from 51 to 64 g kg⁻¹. Wood et al. (1991a) reported a range

from 39 to 68 g kg⁻¹ of β -glucan content of 11 North American cultivars. Lim et al. (1992) analyzed a wider selection of genotypes; 102 lines including commercial cultivars, experimental lines, and accessions of *A. sterilis*. The groat β -glucan concentration ranged from 38 to 61 g kg⁻¹.

Similar values of β -glucan concentrations from oat genotypes grown in other countries have been reported. Welch and Lloyd (1989) analyzed a set of 100 genotypes that primarily included European cultivars. They found a range of β -glucan content from 32 to 63 g kg⁻¹. Saastamoinen et al. (1992) reported a range from 40 to 63 g kg⁻¹ of β -glucan content among varieties and breeding lines grown in Finland.

Barley has concentrations of β -glucan comparable to those from oat. Barley cultivars expressing the hull-less trait and/or waxy endosperm usually contain greater β -glucan concentration than the normal types (Fastnaught et al., 1996). Ulrich et al. (1986) evaluated four normal and waxy barley isoline pairs for β -glucan content. He reported an average content of 48 g kg⁻¹ with a range from 38 to 57 g kg⁻¹ for the normal types and an average of 64 g kg⁻¹ with a range from 47 to 71 g kg⁻¹ for the waxy isotypes. Even though oat and barley have similar β -glucan concentration, oat generally has a larger proportion of soluble β -glucan. Lee et al. (1997) reported an average content of soluble β -glucan of 34 g kg⁻¹ and a range from 25 to 44 g kg⁻¹ among nine barley genotypes adapted to the Northern Great Plains region of the U.S. In oat, the average was 42 g kg⁻¹, with a range from 36 to 50 g kg⁻¹ among 10 genotypes adapted to the same geographical area.

Other cereals have considerably lower concentrations of β -glucan. The β -glucan content usually ranges from 5 to 14 g kg⁻¹ for wheat, from 12 to 23 g kg⁻¹ for rye, and

averages about 12 g kg⁻¹ for triticale and 10 g kg⁻¹ for sorghum (Prentice et al., 1980; Saastamoinen et al., 1989a; Berenford and Stone, 1983).

Genotypic and Environmental Effects on β -Glucan Content

In order to successfully develop oat cultivars with greater β -glucan content, it is helpful to determine the available genetic variation for the trait, its heritability, the effect of the environment, the genotype-by-environment interaction, and its correlations with other traits (Peterson et al., 1995; Brunner and Freed, 1994). The wide ranges in β -glucan content of commercial oat cultivars and breeding lines averaged across environments mentioned in the previous section indicate that there is genetic variation in oat β -glucan content (Holthaus et al., 1996; Lim et al., 1992; Welch and Lloyd, 1989). Some studies have demonstrated a normal distribution of the frequency of oat genotypes for β -glucan concentration (Lim et al., 1992; Welch and Lloyd, 1989) indicating that the oat β -glucan content might be under polygenic control (Falconer and Mackay, 1996). Holthaus et al. (1996) developed seven progeny generations from biparental crosses between oat lines with contrasting β -glucan content. After performing a generation means analysis they found that the concentration of β -glucan is under polygenic control of genes with mainly additive effects and no intergenic interaction. Reciprocal crosses showed evidence of no cytoplasmic effects. They also reported a broad sense heritability of 0.55 estimated on single plant basis using parent-offspring regression. Kibite and Edney (1998) performed generation mean analysis of five generations developed from biparental crosses, finding that β -glucan concentration is under the control of a minimum of two or three genes with predominantly additive effects. They

reported that broad sense heritability ranged from 0.45 to 0.58 in the F_2 generation and from 0.48 to 0.56 in the F_3 generations.

Several studies have demonstrated significant differences in β -glucan concentration among environments. This has been generally observed when the environments are highly diverse (Aman et al., 1989; Brunner and Freed, 1994; Peterson et al., 1995). Although the effects of specific environmental variables on β -glucan content are not known, some associations have been proposed. For example, drought has been related with greater concentrations of β -glucan. Peterson (1991) found significant differences of β -glucan content of 12 oat cultivars among locations in a one year evaluation. He reported that greater concentrations of β -glucan were observed in dry-land conditions than under irrigation. Brunner and Freed (1994) found lower mean β -glucan concentrations in years with high precipitation during the grain filling periods. Fastnaught et al. (1996) reported that a greater mean content of barley β -glucan was observed in a low moisture year than in a high moisture one. Nevertheless, other authors have found evidence against the relation of drought and β -glucan. Lim et al. (1992) did not find differences in the β -glucan mean content of two years when one year was drier and hotter than the other. Peterson et al. (1995) evaluated 33 genotypes for 3 years under irrigation and dry conditions in the same locations as Peterson (1991). However, this time they did not find a consistent advantage of dry over irrigated conditions for β -glucan content. They suggested that other environmental conditions might have more influence on the concentration of β -glucan than drought.

β -Glucan content has also been associated with soil nitrogen level. Welch et al. (1991) found that increasing nitrogen fertility levels applied at seeding stage increased the

kernel β -glucan content of six oat cultivars. They reported that the differences in β -glucan concentrations among cultivars were greater at lower nitrogen levels. Similar results were reported by Brunner and Freed (1994), indicating that soil nitrogen is an important determinant of oat β -glucan content. Humphreys et al. (1994) reported that β -glucan content does not respond to additional nitrogen fertilizer when this is applied in later stages of plant development.

Significant genotype-by-environment interaction for β -glucan content has been reported by Peterson et al. (1995), Brunner and Freed (1994), and Saastamoinen et al. (1992). Nevertheless, Peterson (1991) found that the ranking of β -glucan content of 12 oat cultivars was consistent across locations. Lim et al. (1992) reported ranking conservation of β -glucan content of genotypes across years. These findings suggest that selection for this trait in one or few locations in one year may be performed with the expectation that the selected genotypes would be also superior in other environments (Fehr, 1987).

The associations of oat β -glucan content with other grain and plant traits are important to plant breeders because selection for one trait might also change other traits (Hallauer and Miranda, 1988). Correlated response might be used to increase β -glucan content by indirect selection, but also may cause changes in unfavorable direction in one or more agronomically important traits when direct selection for β -glucan is practiced. Low positive and negative phenotypic correlations and no correlation of β -glucan content with grain yield have been reported (Kibite and Edney, 1998; Holthaus et al., 1996; Peterson et al., 1995; Saastamoinen et al., 1992). It has also been observed that phenotypic correlations of β -glucan with yield can be positive or negative depending of the environment (Brunner and

Freed, 1994). β -Glucan content has exhibited low positive or non-significant correlation with test weight, protein, and groat percentage (Kibite and Edney, 1998; Holthaus et al., 1996; Peterson et al., 1995; Brunner and Freed, 1994; Welch and Lloyd, 1989). However, some workers have found relatively high positive and negative correlations of β -glucan concentration with protein (Welch et al., 1991; Saastamoinen et al., 1992). β -Glucan concentration has been found to be negatively correlated with oil content (Kibite and Edney, 1998; Welch and Lloyd, 1989). Negative and non-significant correlations of β -glucan content and groat weight have been reported (Holthaus et al., 1996; Brunner and Freed, 1994; Welch and Lloyd, 1989). Brunner and Freed (1994) attributed the negative correlation of β -glucan content and groat weight to a greater ratio of cell wall to cell content in small groats. Groat β -glucan content tends to show no association with heading date and plant height (Holthaus et al., 1996; Saastamoinen et al., 1992; Welch and Lloyd, 1989), although some negative correlations have been reported (Peterson et al., 1995).

Estimation of Genetic Components of Variance and Covariance

The total phenotypic variance (σ_p^2) of a population can be partitioned as $\sigma_p^2 = \sigma_G^2 + \sigma_E^2 + \sigma_{GE}^2$, where σ_G^2 is the genotypic variance, σ_E^2 is the environmental variance, and σ_{GE}^2 is the variance due to the interaction of genotypes with environments (Falconer and Mackay, 1996). The genetic variance can be partitioned into variances due to allelic main effects and interactions. To do this, the value of a genotype affected by a single locus is written as $G_{ij} = \mu + \alpha_i + \alpha_j + \delta_{ij}$, where α_i represents the average effect of allele i , and δ_{ij} is the dominance deviation (or interaction effect) of alleles i and j . When the population is in

random-mating Hardy-Weinberg equilibrium, there is no correlation between the two allelic effects at a locus, nor is there a correlation between additive and dominant effects at the locus, so the genotypic variance due to a single locus is: $\sigma_G^2 = E(G_{ij} - \mu)^2 = 2 [E(\alpha^2)] + E(\delta^2) = \sigma_A^2 + \sigma_D^2$, where σ_A^2 is the additive variance and σ_D^2 is the dominance variance.

When the population is not in Hardy-Weinberg equilibrium, however, the allelic effects within a locus are no longer independent. Breeding populations of self-pollinated crops such as oat are frequently not in Hardy-Weinberg equilibrium because they are often inbred to some extent, measured by the inbreeding coefficient, F , the probability that the two alleles at a locus are identical by descent (Falconer and Mackay, 1996). Under inbreeding, the average effects of the two alleles at a locus are correlated, homozygous dominance deviations (δ_{ii}) become more frequent, heterozygous dominance deviations (δ_{ij}) become less frequent, and there can be correlations between additive and homozygous dominant effects within a locus. The total genotypic variance of a population inbred to an inbreeding coefficient of F without selection is:

$$\sigma_G^2 = (1+F)\sigma_A^2 + (1-F)\sigma_D^2 + 4F \sum_i p_i \alpha_i \delta_{ii} + F \sum_i p_i \delta_{ii}^2 - \left(F \sum_i p_i \delta_{ii} \right)^2,$$

where p_i represents the frequency of allele i , and δ_{ii} is the dominance deviation of the homozygous genotype $A_i A_i$ (Weir and Cockerham, 1977). Inbreeding changes the population variance. If $F=0$ the genetic variance is $\sigma_G^2 = \sigma_A^2 + \sigma_D^2$ and if $F=1$ then the genetic variance becomes:

$$\sigma_G^2 = 2\sigma_A^2 + 4\sum_i p_i \alpha_i \delta_{ii} + \sum_i p_i \delta_{ii}^2 - \left(\sum_i p_i \delta_{ii} \right)^2$$

When two or more independent loci are in linkage equilibrium and no inbreeding is involved, the genetic variance is the sum of the individual additive and dominance variances of each locus. If alleles of different loci interact, however, independence is not achieved, and the total genetic variation is not simply the sum of the genetic variation due to each locus. The interallelic interaction can be additive x additive (AA), additive x dominance (AD), dominance x dominance (DD), additive x additive x additive (AAA) and so on. The variances due to these interactions compose the epistatic variance (σ_I^2) which is included in the total genetic variance (Wricke and Weber, 1986).

Some characters in a population can be correlated. The correlation can be due to genetic or environmental effects or both. The genetic correlation is caused by either or both of pleiotropy, in which the same gene controls different traits, or linkage, when traits are controlled by different genes, but the loci are genetically linked (Falconer and Mackay, 1996). Mode and Robinson (1959) partitioned the genetic covariance of the traits W and Z in a random mating population ($F=0$) as $\sigma_{Gwy} = \sigma_{Awy} + \sigma_{Dwy} + \sigma_{AAwz} + \sigma_{ADwy} + \sigma_{Ddwy} + \dots$, where σ_{Gwy} is the genetic covariance between the traits W and Z, σ_{Awy} is the additive covariance, σ_{Dwy} is the dominance covariance and the sum $\sigma_{AAwz} + \sigma_{ADwy} + \sigma_{Ddwy} + \dots$ represents the epistatic covariance. Thus, the genetic covariance between traits is represented with a structure similar to that of the genetic variance of a single trait.

The covariance between relatives can be used to estimate genetic components of variance and covariance (Falconer and Mackay, 1996). The covariance between two

individuals X and Y with genotypes A_iA_j and A_kA_l , respectively, from a population is represented by:

$$C_{XY} = 2\theta_{XY}\sigma_A^2 + 2\delta_{\bar{X}+\bar{Y}}\sigma_D^2 + 2(\gamma_{\bar{X}\bar{Y}} + \gamma_{i\bar{X}\bar{Y}})\sum_i p_i \alpha_i d_{ii} + \delta_{\bar{X}\bar{Y}} \sum_i p_i d_{ii}^2 + (\delta_{\bar{X}\bar{Y}} - F_X F_Y) \left(\sum_i p_i d_{ii} \right)^2,$$

(Weir and Cockerham, 1977) where:

$$\theta_{XY} = (1/4) [p(A_i \equiv A_k) + p(A_i \equiv A_l) + p(A_j \equiv A_k) + p(A_j \equiv A_l)],$$

$$\gamma_{\bar{X}\bar{Y}} = (1/2) [p(A_i \equiv A_j \equiv A_k) + p(A_i \equiv A_j \equiv A_l)], \quad \delta_{\bar{X}\bar{Y}} = p(A_i \equiv A_j \text{ and } A_k \equiv A_l)$$

$$\delta_{\bar{X}+\bar{Y}} = (1/2) [p(A_i \equiv A_k \text{ and } A_j \equiv A_l) + p(A_i \equiv A_l \text{ and } A_j \equiv A_k)] \text{ where } A_i \neq A_j, \text{ and}$$

$$\delta_{\bar{X}\bar{Y}} = p(A_i \equiv A_k \equiv A_j \equiv A_l) \text{ given that the symbol } \equiv \text{ means identity by descent (Malecot,}$$

1948) and F_X and F_Y are the inbreeding coefficients of X and Y, respectively. When X and Y are not inbred, their covariance reduces to the expression:

$$C_{XY} = 2\theta_{XY}\sigma_A^2 + 2\delta_{\bar{X}+\bar{Y}}\sigma_D^2.$$

The coefficients of the additive and dominance variances are determined by the degree of relationship, because the relationship between the individuals determines the probability of the identity by descent gene measures (θ , γ , and δ). Some examples are $\text{cov(OP)} = (1/2)\sigma_A^2$, $\text{cov(FS)} = (1/2)\sigma_A^2 + (1/4)\sigma_D^2$ and $\text{cov(HS)} = (1/4)\sigma_A^2$, corresponding to the covariances of offspring and parent, full sibs, and half sibs, respectively (Falconer and Mackay, 1996).

The covariance between relatives can be also represented in terms of genetic components of covariance between traits W and Z in a random mating population with a structure similar to that of the variance components. The covariance between an individual X measured in trait W and an individual Y measured in trait Z in a random-mating population is given by:

$$C_{.XW.YZ} = 2\theta_{.XY}\sigma_{.AWZ} + 2\delta_{.X+Y}\sigma_{.DWZ}.$$

For example, $\text{cov}(X_w Y_z) = (1/2)\sigma_{Awz} + (1/4)\sigma_{Dwz}$ if X and Y are full sibs and $\text{cov}(X_w Y_z) = (1/4)\sigma_{Awz}$ if X and Y are half sibs (Hallauer and Miranda, 1988; Mode and Robinson, 1959). Thus, the covariance between outbred relatives is represented by linear functions of the additive and dominance variances or by linear functions of the additive and dominance covariance components (Schnell, 1963). Solving a set of these functions for the variance components results in linear functions of the covariance among relatives. The same applies for genetic components of covariance.

Genetical experiments to estimate components of variance and covariance consist of a mating design and an experimental design. Relatives of different degrees of relationship are generated by a mating system or mating design, then they are evaluated in different environments based on an experimental design (Cockerham, 1963). The statistical components of variance and covariance are interpreted in terms of covariances between relatives and from there in terms of components of genetic variance (Hinkelmann, 1975).

The most common mating designs are those that can be analyzed by standard statistical methods (Cockerham, 1963). The Designs I, II and III are popular mating designs

in plant breeding (Hallauer and Miranda, 1988; Hinkelmann, 1975). For example, in the Design I or nested design (Comstock and Robinson, 1948), males taken at random from a population are mated with females also taken at random from the same population. Each male is mated with a different set of females. The number of females per male is the same for all males. If the progeny are evaluated in only one environment using a completely randomized design, the corresponding linear model would be $Y_{ijk} = \mu + m_i + f_{j(i)} + e_{k(ij)}$, $i = 1, 2, \dots, a, j = 1, 2, \dots, b, k = 1, 2, \dots, r$, where Y_{ijk} is the observed value, μ is the general mean, m_i is the effect of the i th male, $f_{j(i)}$ is the effect of the j th female crossed with i th male and $e_{k(ij)}$ is the experimental error. The last three terms are considered random factors with $E(m_i) = E(f_{j(i)}) = E(e_{k(ij)}) = 0$, $\text{var}(m_i) = \sigma_m^2$, $\text{var}(f_{j(i)}) = \sigma_f^2$, and $\text{var}(e_{k(ij)}) = \sigma^2$. The $\text{cov}(Y_{ijk}, Y_{lmn})$ is equal to $\sigma^2 + \sigma_f^2 + \sigma_m^2$ if $i = l, j = m$, and $k = n$. If $i = l, j = m, k \neq n$, then $\text{cov}(Y_{ijk}, Y_{lmn})$ is equal to $\sigma_f^2 + \sigma_m^2$. If $i = l, j \neq m, k \neq n$, then $\text{cov}(Y_{ijk}, Y_{lmn})$ is equal to σ_m^2 . If $i \neq l, j \neq m, k \neq n$, then $\text{cov}(Y_{ijk}, Y_{lmn})$ is equal to 0.

Assuming no inbreeding and no epistasis, there is a simple relationship between the statistical and genetic variance components. If $i = l, j = m, k \neq n$, then $\text{cov}(Y_{ijk}, Y_{ijn})$ equals $\sigma_f^2 + \sigma_m^2$, as noted previously, and in this case Y_{ijk}, Y_{ijn} are full-sibs with both male and female parents in common, so their covariance also must equal $(1/2)\sigma_A^2 + (1/4)\sigma_D^2$. If $i = l, j \neq m, k \neq n$, then $\text{cov}(Y_{ijk}, Y_{ijn})$ equals σ_m^2 , as noted previously, and in this case Y_{ijk}, Y_{ijn} are half-sibs with the male parent in common, so their covariance also must equal $(1/4)\sigma_A^2$. Summarizing these results, we find that:

$$\text{cov}(\text{FS}) = (1/2) \sigma_A^2 + (1/4) \sigma_D^2 = \text{cov}(Y_{ijk}, Y_{ijn}) = \sigma_f^2 + \sigma_m^2$$

$$\text{cov}(\text{HS}) = (1/4) \sigma_A^2 = \text{cov}(Y_{ijk}, Y_{imn}) = \sigma_m^2$$

From this, the components of genetic variance can be expressed in terms of statistical variances: $\sigma^2_A = 4\sigma^2_m$ and $\sigma^2_D = 4(\sigma^2_f - \sigma^2_m)$ (Hallauer and Miranda, 1988). With a similar argument and using covariances instead of variances, the components of genetic covariance are expressed in terms of statistical covariances as $\sigma_{Awz} = 4\sigma_{mwz}$ and $\sigma_{Dwz} = 4(\sigma_{fwz} - \sigma_{mwz})$ (Mode and Robinson, 1959). It follows that estimates of components of genetic variance and covariance can be obtained as linear functions of estimates of statistical variance.

The method of moments, maximum likelihood (ML), and restricted maximum likelihood (REML) are the primary methods to estimate components of variance (Kempthorne, 1969; Searle, 1971). The method of moments consists of conducting an ordinary least squares analysis of variance (ANOVA), equating the mean squares with their expectations obtained using the variance component model and solving the equations for the components of variance. These kinds of estimators are also called ANOVA estimators. For example, the linear model in matrix notation for Design I is $\mathbf{y} = \mathbf{J}\mu + \mathbf{X}_1\mathbf{m} + \mathbf{X}_2\mathbf{f} + \mathbf{e}$, where \mathbf{y} is the vector of observations, \mathbf{J} is a vector of ones, μ is the general mean, \mathbf{X}_1 and \mathbf{X}_2 are association matrices (or design matrices), \mathbf{m} , \mathbf{f} , and \mathbf{e} are vectors that contain the random effects of males, females and error, respectively. The expectancy and variance of the model are $E(\mathbf{y}) = \mathbf{J}\mu$, $\text{var}(\mathbf{y}) = \sigma^2_m\mathbf{X}_1\mathbf{X}_1' + \sigma^2_f\mathbf{X}_2\mathbf{X}_2' + \sigma^2\mathbf{I}$ (Hocking, 1985; Searle, 1971). The expectancy of the mean squares with balanced data for males, females within males and error are $E(\text{MS}_m) = \sigma^2 + r\sigma^2_f + rb\sigma^2_m$, $E(\text{MS}_{f|m}) = \sigma^2 + r\sigma^2_f$, and $E(\text{MS}_e) = \sigma^2$, respectively. The method of moments estimators of the components of variance are the following (Comstock and Robinson, 1948):

$$\hat{\sigma}_m^2 = (MS_m - MS_{f/m})/rb, \hat{\sigma}_f^2 = (MS_{f/m} - MS_e)/r, \text{ and } \hat{\sigma}^2 = MS_e.$$

The expectations of the different sources of variation depend on whether specific model effects are considered random or fixed, but for the purposes of computations, the ordinary least squares ANOVA treats random model effects as if they were fixed.

The components of covariance can also be estimated with the method of moments. The covariance estimates are obtained with a similar procedure, but using mean cross-products of the multivariate ANOVA (MANOVA) instead of mean squares of the ANOVA. The estimates of the genetic covariance between the traits W and Z for Design I are (Mode and Robinson, 1959):

$$\hat{\sigma}_{mWZ} = (MP_{mWZ} - MP_{f/mWZ})/rb, \hat{\sigma}_{fWZ} = (MP_{f/mWZ} - MP_{eWZ})/r \text{ and } \hat{\sigma}_{eWZ} = MP_{eWZ}.$$

Assuming normality of the random effects and independence of the mean squares (which requires balanced data), the sampling variance of a variance estimator of the form $\sum c_i MS_i$ is given by:

$$\hat{\sigma}_{\hat{\sigma}^2}^2 = 2 \sum_i (c_i^2 MS_i^2 / (df_i + 2)),$$

where the c_i 's are constants, and df_i and MP_i are the degrees of freedom and mean square,

respectively, of the corresponding source of variation. The sampling variance of a covariance estimator of the form $\sum c_i MP_i$, where MP_i is the mean product of the corresponding source of covariation, is obtained with the formula:

$$\hat{\sigma}_{\hat{\sigma}_{cov}}^2 = 2 \sum_i (c_i^2 MP_i^2 / (df_i + 2))$$

(Mode and Robinson, 1959; Satterthwaite, 1946).

The ANOVA methods may produce negative estimates of variance components (Hocking, 1985). For balanced data, the method of moments estimators are the uniformly best quadratic unbiased estimators. If the data are normal, then the ANOVA estimators are the uniformly best unbiased estimators (Graybill and Wortham, 1956). When data are unbalanced, these estimators are no longer the uniformly best unbiased estimators. Furthermore, since the means squares may not be independent, the equation given by Satterthwaite (1946) to estimate the variance of the estimator may no longer apply. Three methods were proposed by Henderson (1953) to compute the expected mean squares for unbalanced data. The method III is the most popular of them. However, there is some concern about the number of equations involved in the application of this method (Hocking, 1985; Anderson, 1979) and little is known about any optimality properties of the resulting estimators (Hartley and Rao, 1967).

The maximum likelihood (ML) method is a probability-dependent method. In general, the idea of this method is to find an estimate of the unknown parameters that maximizes the probability of obtaining the observed data (Freud, 1992). The linear model used in this case is a mixed model. Searle (1971) presents the mixed model in matrix notation as $\mathbf{y} = \mathbf{XB} + \mathbf{Zu} + \mathbf{e}$, where \mathbf{y} is a vector of observed responses, \mathbf{X} and \mathbf{Z} are association matrices, \mathbf{B} is a vector of fixed effects, \mathbf{u} is a vector of random model effects, and \mathbf{e} is a vector of random residual error effects. \mathbf{Zu} is partitioned as $\sum \mathbf{Z}_i \mathbf{u}_i$, where \mathbf{u}_i represents a vector of random effects for the i th factor and \mathbf{Z}_i is the corresponding association matrix. The assumptions of the model are $E(\mathbf{u}_i) = \mathbf{0}$, $\text{var}(\mathbf{u}_i) = \sigma_i^2 \mathbf{I}$, $E(\mathbf{e}) = \mathbf{0}$, $\mathbf{Z}_0 = \mathbf{I}$, $\text{var}(\mathbf{e}) = \sigma_0^2 \mathbf{I} = \mathbf{Z}_0 \sigma_0^2$, $\text{cov}(\mathbf{u}_i, \mathbf{u}_j) = \mathbf{0}$ for $i \neq j$, $\text{cov}(\mathbf{u}_i, \mathbf{e}) = \mathbf{0}$, $E(\mathbf{y}) = \mathbf{XB}$ and $\text{var}(\mathbf{y}) = \mathbf{V} = \sum \mathbf{Z}_i \mathbf{Z}_i' \sigma_i^2$. The data

are also assumed to have normal distribution. The likelihood function is the sampling distribution as a function of the unknown parameters in the matrices **B** and **V** as follows:

$$L = (2\pi)^{-n/2} |\mathbf{V}|^{-1/2} \exp\left[(-1/2)(\mathbf{y} - \mathbf{XB})' \mathbf{V}^{-1} (\mathbf{y} - \mathbf{XB})\right].$$

The maximum likelihood estimators are the values of **B** and **V** that maximize the likelihood of *L*. The maximization of *L* is achieved by differentiating the log *L* with respect to **B** and **V**, equating the derivatives to zero to obtain the ML equations, and solving them for **B** and σ_i^2 's. Solving the ML equations generally requires iterative numerical methods. Only in special cases are closed expressions of the ML equations obtained. When negative values for variance components are obtained, they are replaced with zeros. The ML estimators of the σ_i^2 's are the solutions to the ML equations that satisfy the non-negative requirement (Searle, 1971; Hartley and Rao, 1967). Although the ML estimators are not generally unbiased, they tend to converge to the parameters when the sample size is increased. The asymptotic variance-covariance matrix of the estimators is estimable, allowing estimation of the sampling variances of the variance component estimates via the delta method. When the sample size is small, such variances of the ML estimators are underestimated (Self and Liang, 1987; Searle, 1971).

The bias of the ML estimators results from not considering the degrees of freedom used for estimating fixed effects when simultaneously estimating the variance components (Searle, 1971). To overcome this problem, the restricted maximum likelihood (REML) method fits the fixed effects first using ordinary least squares and then maximizes the likelihood function of the residuals with respect to the σ_i^2 's (Mrode, 1996). The ordinary least squares solution to the fixed effects of the mixed model are given by the expression:

$\mathbf{b} = (\mathbf{X}'\mathbf{X})^{-1} \mathbf{X}'\mathbf{y}$. The adjusted values are represented as follows:

$$\hat{\mathbf{y}} = \mathbf{X}\mathbf{b} = \mathbf{X}(\mathbf{X}'\mathbf{X})^{-1} \mathbf{X}'\mathbf{y} = \mathbf{P}_X \mathbf{y} \text{ and } \mathbf{P}_X \mathbf{X} = \mathbf{X}(\mathbf{X}'\mathbf{X})^{-1} \mathbf{X}'\mathbf{X} = \mathbf{I},$$

where \mathbf{P}_X is a projection matrix (Hocking, 1985). The residuals are given by:

$$\mathbf{y} - \hat{\mathbf{y}} = \mathbf{y} - \mathbf{P}_X \mathbf{y} = (\mathbf{I} - \mathbf{P}_X) \mathbf{y} = \mathbf{k}' \mathbf{y} \text{ and } \mathbf{k}' = \mathbf{I} - \mathbf{P}_X.$$

The expectancy and variance of the residuals are:

$$E(\mathbf{k}' \mathbf{y}) = E(\mathbf{y} - \hat{\mathbf{y}}) = \mathbf{P}_X E(\mathbf{y}) = \mathbf{P}_X \mathbf{X} \mathbf{b} = \mathbf{0} \text{ and } \text{var}(\mathbf{k}' \mathbf{y}) = \mathbf{k}' \text{var}(\mathbf{y}) \mathbf{k} = \mathbf{k}' \mathbf{V} \mathbf{k} \text{ respectively.}$$

Under the assumptions of normality of the mixed model, $\mathbf{k}' \mathbf{y}$ has a normal distribution that does not depend on \mathbf{B} . The REML equations are obtained by maximizing the restricted likelihood function of $\mathbf{k}' \mathbf{y}$. The solutions of the REML equations are the REML estimators of the σ^2_i 's. The solutions are obtained generally by numerical methods (Littell et al., 1996; Mrode, 1996; Searle, 1971). For both balanced and unbalanced data, the REML estimators are consistent, and asymptotically normally distributed and their asymptotic sampling variance-covariance matrix is always known. For balanced data, the REML estimators are the same as the ANOVA estimators, when the ANOVA estimators are non-negative (Searle, 1971).

Estimation of Heritability and Genetic Correlation

Quantifying the amount of the different types of variation in a population is an important step in a plant selection program because not all components of the total variability contribute in the same way to selection response (Dickerson, 1963). The environmental variance is composed of all the non-genetic differences among individuals in a population (Falconer and Mackay, 1996). The effects of environments on genotypes may not be

maintained from one environment to another (Hallauer and Miranda, 1988). The genotype-by-environment variance component does not contribute to selection response observed in different environments (Dickerson, 1963).

Response to selection results when selection is practiced on individuals or families with different genotypic values. The variation among genotypic values makes up the genotypic variance, as discussed previously (Falconer and Mackay, 1996; Fehr, 1987). The proportion of the total variance that is due to total genotypic variance is called heritability in broad sense and is denoted by $H^2 = \sigma_G^2 / \sigma_P^2$ (Falconer and Mackay, 1996). The breeding value is the proportion of the genotype that is transmitted from parents to offspring. The variance of breeding values is what is known as additive variance and contributes fully to selection response (Falconer and Mackay, 1996; Dickerson, 1963). The ratio of additive variance to phenotypic variance is called heritability in narrow sense and is denoted as $h^2 = \sigma_A^2 / \sigma_P^2$ (Falconer and Mackay, 1996).

The terms included in the phenotypic variance depend on the number of environments used in the experiment to estimate heritability. When single plants are measured in only one environment, the phenotypic variance is expressed as $\sigma_P^2 = \sigma_G^2 + \sigma_e^2 + \sigma_w^2$, where σ_e^2 is the plot to plot variance and σ_w^2 is the within-plot variance (Fehr, 1987). The broad sense heritability estimated on the bases of single plants, plot means, and entry means are:

$$\hat{H}^2 = \hat{\sigma}_G^2 / (\hat{\sigma}_G^2 + \hat{\sigma}_e^2 + \hat{\sigma}_w^2), \hat{H}^2 = \hat{\sigma}_G^2 / [\hat{\sigma}_G^2 + \hat{\sigma}_e^2 + (\hat{\sigma}_w^2 / n)]$$

and $\hat{H}^2 = \hat{\sigma}_G^2 / [\hat{\sigma}_G^2 + (\hat{\sigma}_e^2 / r) + (\hat{\sigma}_w^2 / rn)]$, respectively, where r is the number of replications

and n is the number of plants per plot. If plants are evaluated in different environments, the phenotypic variance becomes $\sigma_p^2 = \sigma_G^2 + \sigma_{GE}^2 + \sigma_e^2 + \sigma_w^2$. The genotype-by-environment interaction variance is represented by σ_{GE}^2 . The broad sense heritabilities estimated on single plant basis, plot mean basis and entry mean basis are:

$$\hat{H}^2 = \hat{\sigma}_G^2 / (\hat{\sigma}_G^2 + \hat{\sigma}_{GE}^2 + \hat{\sigma}_e^2 + \hat{\sigma}_w^2), \hat{H}^2 = \hat{\sigma}_G^2 / [\hat{\sigma}_G^2 + \hat{\sigma}_{GE}^2 + (\hat{\sigma}_e^2 / r) + (\hat{\sigma}_w^2 / rn)] \text{ and}$$

$$\hat{H}^2 = \hat{\sigma}_G^2 / [\hat{\sigma}_G^2 + (\hat{\sigma}_{GE}^2 / l) + (\hat{\sigma}_e^2 / lr) + (\hat{\sigma}_w^2 / lrn)], \text{ respectively.}$$

Narrow sense heritability is obtained by including only the additive component of the genetic variance in the numerator of the heritability formula (Hallauer and Miranda, 1988; Dickerson, 1963). Exact confidence intervals for heritability estimates can be constructed for some experimental designs with balanced data under the assumption of normality of data (Knapp, 1986; Knapp et al., 1985). Holland and Cervantes-Martinez (2000) derived the standard errors for heritability estimates constructed from REML estimates of variance components.

When two traits are associated, selecting for one trait may causes changes in the other trait; this is referred to as a correlated response (Hallauer and Miranda, 1988). The association between traits is measured in terms of correlation. The phenotypic correlation is partitioned into genetic and environmental correlations (Falconer and Mackay, 1996). The additive correlation is the most important component of the genotypic correlation because only it contributes to correlated response from selection (Hallauer and Miranda, 1988; Falconer and Mackay, 1996). The covariance between the traits W and Z is represented as $\sigma_{Awz} = \sigma_{Awz} + \sigma_{Ewz}$, where σ_{Awz} is the additive covariance and σ_{Ewz} is the environmental (non-

additive) covariance. The phenotypic and additive correlation are given by (Falconer and Mackay, 1996):

$$r_{P_{WZ}} = \sigma_{P_{WZ}} / \sqrt{\sigma_{P_W}^2 \sigma_{P_Z}^2} \text{ and } r_{A_{WZ}} = \sigma_{A_{WZ}} / \sqrt{\sigma_{A_W}^2 \sigma_{A_Z}^2}$$

The correlation estimators are obtained by substituting the variances and covariances with their respective estimators. The amount of the additive covariance in the formula depends on the family structure used in the analysis. For example, the estimator of the additive correlation between the traits W and Z of half sibs in Design I is represented as (Hallauer and Miranda, 1988):

$$r_{A_{WZ}} = (1/4)\sigma_{A_{WZ}} / \sqrt{(1/4)^2 \sigma_{A_W}^2 \sigma_{A_Z}^2} = \sigma_{A_{WZ}} / \sqrt{\sigma_{A_W}^2 \sigma_{A_Z}^2} .$$

CHAPTER 3. SELECTION FOR GREATER β -GLUCAN CONTENT IN OAT GRAIN

A paper to be submitted to *Crop Science*

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Abstract

Oat (*A. sativa* L.) β -glucan lowers serum cholesterol in humans. Development of oat cultivars with greater groat β -glucan content would increase the nutritional and economic value of the crop. The response to phenotypic selection among individual S_0 plants for greater β -glucan content in two genetically broad-based populations was determined by evaluating random $S_{0:1}$ lines from initial and selected generations of each population in a field experiment in 1996 and 1997 at two Iowa locations. The mean β -glucan content increased from 54.0 g kg⁻¹ to 59.8 g kg⁻¹ in one first population, and from 63.5 g kg⁻¹ to 66.1 g kg⁻¹ in the second population. Its genetic variance decreased 9.3% and 21.8% in the two populations, respectively. Heritability estimates ranged from 0.49 to 0.65 on a sample-basis and from 0.80 to 0.88 on a line mean-basis. Additive variance was the only substantial component of

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genetic variance. Ranking of $S_{0.1}$ lines for β -glucan content across environments was generally consistent, with correlations of genotypic β -glucan contents between pairs of environments ranging from 0.63 to 0.82. Some experimental lines had significantly greater β -glucan content than the best check cultivars and lines. Phenotypic selection for greater groat β -glucan content will be effective for developing cultivars with elevated β -glucan contents.

Introduction

Serum cholesterol levels are strongly related to coronary heart disease risk in humans (Mayes, 1990; Shekelle et al., 1981). Greater levels of high-density lipoprotein cholesterol (HDL-C) are related to lower incidence of coronary heart disease, whereas greater levels of low-density lipoprotein cholesterol (LDL-C) are associated with greater levels of coronary heart disease (Castelli et al., 1986; Stamler, 1979; Miller et al., 1977). Soluble fiber has the potential to reduce serum cholesterol levels in humans (Shinnick et al., 1991; Van Horn et al., 1988; Jenkins et al., 1975). Oat (*Avena sativa* L.) bran and oatmeal have been intensively studied as sources of dietary fiber for human diets (Sacks, 1991). Oat soluble fiber, when added to the daily diet, tends to lower serum LDL-C and total blood cholesterol, particularly in individuals with initially greater levels of serum cholesterol (Welch, 1995; Ripsin et al., 1992; Shinnick et al., 1991; Anderson et al., 1984). This results in a reduction of the risk of coronary heart disease. The (1→3),(1→4)- β -D-glucan (β -glucan) has been identified as the active component of soluble fiber that lowers serum cholesterol (Davidson et al., 1991; Klopfenstein and Hosney, 1987).

β -glucan is a cell wall polysaccharide found in seeds of the Gramineae (Stinard and Nevins, 1980; Nevins et al., 1978). Among cereals, oat and barley (*Hordeum vulgare* L.) have the highest concentrations of β -glucan (Wood, 1994; Åman and Hesselman, 1985; Prentice et al., 1980), but oat generally has a larger proportion of soluble β -glucan (Lee et al., 1997). In oat and barley grains, β -glucan is found mainly in the endosperm and the subaleurone layer (Wood, 1993; Wood et al., 1983). Lim et al. (1992) reported that the groat β -glucan content ranged from 38 to 61 g kg⁻¹ among 102 oat lines, including commercial cultivars, experimental lines, and accessions of the wild, interfertile oat relative *A. sterilis* L.

Holthaus et al. (1996) reported that oat β -glucan content is a polygenic trait under the control of genes with mainly additive effects and no interallelic interaction. They estimated broad sense heritability to be 0.55 on single plant-basis using parent-offspring regression. Kibite and Edney (1998) performed generation mean analysis of five generations developed from biparental crosses, finding that oat β -glucan content is under the control of a minimum of two or three genes with predominantly additive effects. They reported that broad sense heritability ranged from 0.45 to 0.58 in the F₂ generation and from 0.48 to 0.56 in the F₃ generation. β -glucan content is affected by environmental factors, including soil nitrogen level (Peterson et al., 1995; Brunner and Freed, 1994; Humphreys et al., 1994; Peterson, 1991; Welch et al., 1991). Although genotype-by-environment interaction sometimes is a significant source of variation for β -glucan content, the ranking of genotypes is generally consistent over environments (Peterson et al., 1995; Brunner and Freed, 1994; Lim et al., 1992; Saastamoinen et al., 1992).

The inheritance of β -glucan and the availability of technology developed to measure the trait rapidly using flow injection analysis (FIA) (Jørgensen, 1988) or near infrared reflectance spectrophotometry (NIRS) (Osborne et al., 1983) make possible the improvement of oat β -glucan content through phenotypic selection. The development of oat cultivars with greater groat β -glucan contents should increase the nutritional and economic value of the oat crop.

The objectives of this study were (1) to develop two genetically broad-based oat populations from parents with greater levels of β -glucan content and to conduct phenotypic selection for greater β -glucan content in these populations, (2) to determine the progress from phenotypic selection of individual S_0 plants for greater β -glucan content, and (3) to determine if additive variance is the predominant component of genetic variance for β -glucan content and to estimate changes in genetic variance and heritability.

Materials and Methods

Two base populations were developed in which to test the effects of selection for greater β -glucan content: IABG1C0 and IABG2C0.

Development of the IABG1C0 base population

The IABG1C0 population was developed by intermating 23 oat breeding lines and commercial cultivars chosen for their high β -glucan content or good agronomic characteristics, followed by two additional generations of intermating unrelated F1 plants.

The S_0 seed obtained from 97 crosses made in the third generation of intermating constituted the base population for selection, IABG1C0 (Figure 1).

Selection within IABG1C0 for greater β -glucan

In 1992, in Aberdeen, Idaho, 1665 S_0 plants (from two to 38 per cross) from IABG1C0 were grown as spaced plants in the field. S_0 plants from the same cross made to obtain the IABG1C0 seed represented a full-sib family. The S_1 seed of each S_0 plant was harvested individually and analyzed for groat β -glucan content via automated flow injection analysis (FIA) as described by Lim et al. (1992). The groat β -glucan content of each plant was estimated by the mean of three subsamples and three individual measurements per subsample. The 40 $C_0 S_{0:1}$ lines with highest β -glucan content represented 21 full-sib families and were selected to be parents of the IABG1C1 population. The 40 parent lines were intermated in the greenhouse in spring of 1993 by crossing each line to approximately six others in circular fashion to obtain 116 single crosses, which together constituted the IABG1C1 population. In 1993, 582 S_0 plants representing the IABG1C1 population were grown as spaced plants in the field at Aberdeen, ID. S_0 plants from each cross made to form IABG1C1 represented a full-sib family. Each plant was harvested individually to form 582 $S_{0:1}$ lines.

Development of the IABG2C0 base population

The IABG2C0 base population was developed primarily by crossing selected lines from the IABG1C1 population with lines from a population (IABGPI) possessing germplasm

from unadapted plant introductions (PIs) with high β -glucan content. The IABGPI population was used as a donor for potentially unique alleles for greater β -glucan content. It was developed by mating S_0 plants from ten crosses with at least 25% PI parentage (Table 1) to the same 40 $S_{0;l}$ lines selected from IABG1C0 that were also used as parents of IABG1C1 (Figure 2).

The choice of lines from the IABG1C1 and IABGPI populations to use as parents for the second base population was made based on β -glucan contents of S_0 plants from the two populations grown together in Aberdeen in 1993. The S_0 plants from each cross made to form the IABG1C1 and IABGPI seed represented a full-sib family. A total of 951 S_0 plants (from one to ten per full sib family) representing the IABG1C1 and IABGPI populations combined were evaluated. Each plant was harvested individually and analyzed for β -glucan content via FIA.

Thirty-eight $S_{0;l}$ lines representing 31 full-sib families from the IABG1C1 population and seven lines from the IABGPI population were selected to be used as parents of IABG2C0 because of their greater β -glucan contents. In addition, 12 high β -glucan experimental lines and the cultivar Marion also were selected to be parents for the IABG2C0 population, giving a total of 50 parents. The 50 parent lines were intermated in the greenhouse in spring of 1994 by crossing each line to approximately 10 others in circular fashion to obtain 248 crosses, which together constituted the IABG2C0 population (Figure 2). The IABG2C0 population is highly related to the IABG1C0 population, but differs from it by the inclusion of PI germplasm and of germplasm from only from the selected lines of IABG1C0 and IABG1C1.

Selection within IABG2C0 for greater β -glucan

In 1994, in Aberdeen, Idaho, 916 IABG2C0 S_0 plants (from one to five per cross) were grown as spaced plants. S_0 plants from the same cross made to form the IABG2C0 seed represented a full-sib family. Each S_0 plant was harvested individually and analyzed for β -glucan content via FIA. A single line with the highest β -glucan content within each of the 50 families out of 248 with the highest mean β -glucan contents was selected to be a parent of the IABG2C1 population. The selected lines were crossed in the greenhouse in spring of 1995 by crossing each line to approximately 10 others in circular fashion. A total of 250 single crosses was made and a total of 1471 S_0 seeds constituted the IABG2C1 population. The IABG2C1 population was grown as spaced plants in Aberdeen, ID in the summer of 1995. S_0 plants from the same cross made to form the IABG2C1 seed represented a full-sib family. Each plant was harvested individually to form 1471 $S_{0,1}$ lines (Figure 2).

Field evaluation

Fifty full-sib families from IABG1C0, IABG2C0 and IABG2C1, 33 full-sib families from IABG1C1 and 17 full-sib families from IABGPI were chosen at random for a field experiment. The IABG1C0, IABG1C1, IABG2C0 and IABG2C1 populations were evaluated to determine the progress from phenotypic selection among individual S_0 plants for greater β -glucan content. The IABGPI population was evaluated to analyze the effect of germplasm developed from unadapted plant introductions with high β -glucan content on the mean and genetic variance of β -glucan content. Each full-sib family was represented by two

randomly-chosen $S_{0,1}$ lines chosen at random, resulting in the inclusion of 400 experimental $S_{0,1}$ lines in the evaluation experiment.

Experimental and check oat lines were evaluated in a field experiment in 1996 and 1997. The experimental design was a sets within replications design. Each replication had five sets. Each set of 100 entries was arranged as a 10 x 10 square lattice with two replications at each environments. The experiment was grown at the Agronomy and Agricultural Engineering Field Research Center near Ames, IA, on a Nicollet loam soil (fine-loamy, mixed, mesic Aquic Hapludoll) and the Northeast Research Center near Nashua, IA, on a Readlyn loam soil (fine-loamy, mixed, mesic Aquic Hapludoll) in both years. The treatment design consisted of five populations (IABG1C0, IABG1C1, IABG2C0, IABG2C1, IABGPI); 100 $S_{0,1}$ lines randomly chosen from each of the IABG1C0, IABG2C0, IABG2C1 populations; and 66 and 34 $S_{0,1}$ lines randomly chosen from the IABG1C1 and IABGPI populations. Lines were randomly assigned to five sets such that each set received 20 lines from each of the IABG1C0, IABG2C0, IABG2C1 populations; 8 to 20 lines from the IABG1C1 population; and zero to 12 lines from the IABGPI population to make a total of 80 experimental lines per set. Twenty check entries were included in each set. Seven commercial oat cultivars (Don, Marion, Hazel, Premier, Ogle, Starter, and Noble) were included in each set in duplicate. Each set also included five of the original parental lines of IABG1C0 or IABGPI (C05406, D831-1-571, D921-255, H52-1, H87-7-4, H688-11, H730-12, IAN979-5-2, IL82-2154, IL85-6183-1, MN88156, MN86226, MO07929, N04-8, NO5-1, N010-1, N011-1, N020-1, OA926-2, P7869D1-5-3, PI412928, PI361884, PI361886,

PI502955, PI504593, or PI504601), which were assigned to sets at random. Each set also included a high β -glucan experimental line, IAN979-5-2.

Field plots consisted of hills of 20 seeds planted on a grid 0.3 m apart. Each experiment was surrounded by two rows of hills of a common check cultivar to provide competition to peripheral plots. Fertilizer consisted of 15-23-23 and 40-0-0 kg ha⁻¹ of nitrogen, phosphorous, and potassium at Ames and Nashua. Weeds were controlled manually. Plots were sprayed with the systemic fungicide Bayleton [1-(4-chlorophenoxy)-3,3-dimethyl-1-(1H-1,2,4-triazol-1-yl)-2-butanone] to protect them from crown rust infection [*Puccinia coronata* (Corda.)]. Each plot was harvested in bulk. To have sufficient seed for spectrophotometry and chemical analysis, the grain from both replications of each entry within a location was bulked together, mixed thoroughly, and the β -glucan content of a representative portion of each sample was estimated.

Grain samples were dehulled using an air pressure dehuller (Codema brand model LH 5095) to obtain approximately 8 g of groats. The β -glucan content of each groat sample was determined with a near-infrared reflectance spectrophotometer (NIRS) (Pacific Scientific Model 6250). The β -glucan value for each sample was the mean of three measurements. β -glucan content of 92 samples from the 1996 evaluation and 95 samples from the 1997 evaluation (representing approximately 10% of the total number of samples from each year) also were measured with the automated flow injection analysis (FIA) as described by Lim et al. (1992) to calibrate the prediction equation for β -glucan content for each evaluation year. The calibration samples were selected on the basis of spectral features to represent the spectral variability of the whole set of samples. A β -glucan determination for a sample

chosen for the calibration equation was the mean of nine values: three subsamples were taken from each sample and three FIA measurements were obtained for each subsample. The prediction equations for each year of evaluation were developed using modified partial least squares (Benson, 1986).

Statistical analysis

To compare population means, an analysis was performed using mixed models analysis, considering the overall mean and populations as fixed effect factors and all other factors random. The analysis was performed on values for β -glucan content of each bulk of grain representing an entry-environment combination. Data were analyzed using PROC MIXED of SAS (Littell et al., 1996). F-tests were performed to test for significant differences among populations. To test the progress of selection for high β -glucan content, contrasts were made between the IABG1C0 and IABG1C1 populations, and between the IABG2C0 and IABG2C1 populations. To make comparisons between specific experimental lines and the checks, a second analysis of variance was conducted using PROC MIXED, but considering entries within sets as a fixed factor and sets and environments as random. Fisher's protected LSDs were obtained for pair-wise comparisons among experimental lines, among checks, and between experimental lines and checks using the restricted maximum likelihood (REML) estimator of the corresponding standard error for mean differences.

The components of variance were estimated by population with the REML method (Searle, 1971). The analysis was performed with PROC MIXED of SAS (Littell et al., 1996) for each population separately, after discarding all checks and considering all effects except

the overall mean to be random. Because of the family structure inherent in each population, we were able to classify lines according to which full-sib family (or cross) they belonged. Each full-sib family sampled was represented by two $S_{0.1}$ lines in the experiment. Therefore, we were able to estimate components of variance due to family and due to line within family for each population. This partitioning of the total genetic variance into among- and within-full-sib family variation allowed us to test the hypothesis that additive genetic variance was the sole component of genetic variance, as follows. Genetic expectations of the family and $S_{0.1}$ line within family variance components were derived following the formulas of Cockerham (1983; 1971). The expectations for these components in the IABG1C0 population were different than in the other populations because the parents of the IABG1C0 population were non-inbred S_0 plants, whereas the parents of IABG1C1, IABG2C0, and IABG2C1 were partially inbred S_1 plants. The genetic expectancies of family and $S_{0.1}$ line within family variance of the IABG1C0 population are:

$$\sigma^2_{\text{family}} = (1/2)\sigma^2_A + (1/32)\sigma^2_D + (1/2)D_1 + (1/16)D_2 + (1/4)\sigma^2_{AA} + (1/32)\sigma^2_{AD} + (1/256)\sigma^2_{DD}$$

and

$$\sigma^2_{\text{line(family)}} = (1/2)\sigma^2_A + (3/16)\sigma^2_D + (1/2)D_1 + (1/16)D_2 + (3/4)\sigma^2_{AA} + (7/32)\sigma^2_{AD} + (15/256)\sigma^2_{DD},$$

where σ^2_A is the additive variance, σ^2_D is the dominance variance, D_1 is the covariance between additive effects and homozygous dominant effects, D_2 is the variance of homozygous dominant effects, and σ^2_{AA} , σ^2_{AD} and σ^2_{DD} are the additive x additive, additive x dominant and dominant x dominant epistatic variances, respectively (Nyquist, 1991). The

expectations of the variance components of family and $S_{0:l}$ line within family variance of the IABG1C1, IABG2C0 and IABG2C1 populations are:

$$\sigma^2_{\text{family}} = (3/4)\sigma^2_A + (9/64)\sigma^2_D + (3/4)D_1 + (3/32)D_2 + (9/16)\sigma^2_{AA} + (27/256)\sigma^2_{AD} + (81/4096)\sigma^2_{DD}$$

$$\sigma^2_{\text{line(family)}} = (1/4)\sigma^2_A + (7/64)\sigma^2_D + (1/4)D_1 + (1/32)D_2 + (7/16)\sigma^2_{AA} + (37/256)\sigma^2_{AD} + (175/4096)\sigma^2_{DD}$$

Under the hypothesis that additive genetic variance is the only substantial component of the genetic variance, the following equalities are true: $\sigma^2_{\text{family}} - \sigma^2_{\text{line(family)}} = 0$ for IABG1C0 and $\sigma^2_{\text{family}} - 3\sigma^2_{\text{line(family)}} = 0$ for the IABG1C1, IABG2C0 and IABG2C1 populations. These equations were tested assuming asymptotic normality of the variance component estimates.

In this analysis the residual variance was the environment-by-line within family component of variance confounded with the error variance. To partition these two components of variance, the error variance was estimated independently as the pooled variance of repeated checks within sets and environments. A contrast of the residual variance vs the error variance was performed assuming asymptotic normality (Self and Liang, 1987; Searle, 1971) to test the significance of the environment-by-line within family variance. Significance tests of the other components of variance were obtained with the likelihood ratio test, which assumes that the difference between the -2 REML log-likelihood of the full model and the reduced model without the component of variance in question has a chi-square distribution with one degree of freedom (Self and Liang, 1987; Littell et al., 1996).

The estimate of the phenotypic variance on a sample-basis was obtained as the sum of family, line within family, and environment-by-family variance components plus the

environment-by-line within family interaction variance confounded with the experimental error variance.

Heritability on a sample-basis was estimated as:

$$H^2 = (\hat{\sigma}_{family}^2 + \hat{\sigma}_{line(family)}^2) / (\hat{\sigma}_{family}^2 + \hat{\sigma}_{line(family)}^2 + \hat{\sigma}_{env \times family}^2 + \hat{\sigma}_{env \times line(family)}^2 + \hat{\sigma}_{error}^2).$$

Heritability on a line mean - basis was estimated as :

$$H^2 = (\hat{\sigma}_{family}^2 + \hat{\sigma}_{line(family)}^2) / [\hat{\sigma}_{family}^2 + \hat{\sigma}_{line(family)}^2 + (\hat{\sigma}_{env \times family}^2 + \hat{\sigma}_{env \times line(family)}^2 + \hat{\sigma}_{error}^2) / 4].$$

Heritability on a family mean-basis was estimated as:

$$H^2 = \hat{\sigma}_{family}^2 / [\hat{\sigma}_{family}^2 + \hat{\sigma}_{line(family)}^2 / 2 + \hat{\sigma}_{env \times family}^2 / 4 + (\hat{\sigma}_{env \times line(family)}^2 + \hat{\sigma}_{error}^2) / 8].$$

The approximate standard errors of these heritability estimates were obtained following

Holland and Cervantes-Martinez (2000). Predicted responses to selection for the IABG1 and the IABG2 populations were obtained with the formula $R = i\sigma_{ph}H^2$, where i is the intensity of selection, and σ_{ph} and H^2 are the phenotypic standard deviation and heritability, respectively (Falconer and Mackay, 1996). Heritability on a sample-basis was used to predict response to selection for IABG1. In the case of the IABG2 population, the total predicted response was obtained as the sum of the response to selection among full-sib families and the response to selection of S_0 lines within full-sib families. On average, each full-sib family consisted of three S_0 lines when selection was performed. The heritabilities relevant to selection among and within full-sib families measured in one environment were estimated as:

$$H^2 = \hat{\sigma}_{family}^2 / [\hat{\sigma}_{family}^2 + \hat{\sigma}_{line(family)}^2 / 3 + \hat{\sigma}_{env \times family}^2 + (\hat{\sigma}_{env \times line(family)}^2 + \hat{\sigma}_{error}^2) / 3] \text{ and}$$

$$H^2 = \hat{\sigma}_{line(family)}^2 / (\hat{\sigma}_{line(family)}^2 + \hat{\sigma}_{env \times line(family)}^2 + \hat{\sigma}_{error}^2), \text{ respectively.}$$

Heritabilities and phenotypic standard deviations were estimated from the evaluation experiments in 1996 and 1997, whereas the intensity of selection was calculated from the original selection trials. T-tests were performed for both populations to test if the realized response to selection fit the predicted response.

To relate mean β -glucan content averaged over all entries within environments to climatic variables, the mean minimum air temperature, maximum air temperature, and precipitation for the pre- and post-flowering periods of each environment were recorded. Mean β -glucan content from each environment was regressed on each climate variable from each period.

Results and Discussion

Prediction equation validation

The coefficient of determination (R^2) of the NIRS prediction equation for β -glucan content was 0.76 for the 1996 evaluation and 0.80 for 1997. The standard error of calibration (SEC) was 4.7 g kg⁻¹ for 1996 and 3.8 g kg⁻¹ for 1997. The SEC describes how well the calibration equation fit the samples. An equation with SEC about twice the standard error of laboratory measurement (SEL) using a standard reference method is generally accepted for use for protein content (Benson, 1986). The SEL obtained with the flow injection analysis

(FIA) was 3.3 g kg⁻¹ in 1996 and 0.6 g kg⁻¹ in 1997. The precision of FIA measurements was much greater in 1997 than in 1996, but this resulted in only a small improvement in the precision of the regression equation.

Response to selection

Selection resulted in significant increases in mean β -glucan content in both populations (Table 2). The mean β -glucan content of the IABG1 population increased from 54.0 g kg⁻¹ in C0 to 59.8 g kg⁻¹ in C1, corresponding to an increase of 11% of the unselected population mean. A smaller increase of 4% was observed in the IABG2 population, which changed from 63.5 g kg⁻¹ in C0 to 66.1 g kg⁻¹ in C1. The original parental lines of the IABG1C0 population had a mean of 54.8 g kg⁻¹, not significantly different from the IABG1C0 mean. This result was expected under the assumption that the β -glucan content is controlled by genes mainly with additive effects (Kibite and Edney, 1998; Holthaus et al., 1996). The mean β -glucan content of check cultivars was not significantly different from the IAB1C0, parental line, and IABGPI means, and was significantly ($P \leq 0.05$) lower than the IABG1C1, IABG2C0 and IABG2C1 means (Table 2).

Lines from the IABG2C0 and IABG2C1 populations generally had greater β -glucan content than lines from IABG1C0 and IABG1C1. This was because the IABG2 population was developed in part from lines selected for greater β -glucan content from the IABG1C1 population. In set one, for example, one line from IABG2C0 and three lines from IABG2C1 had significantly greater mean β -glucan contents than the check with highest β -glucan content, experimental line IAN979-5-2 (Table 3). The 10 lines with highest mean β -glucan

content in set one were significantly greater in β -glucan percentage than all of the commercial checks (Starter, Hazel, Noble, Don, and Ogle). Similar trends were observed in the other four sets.

The range of mean β -glucan content across environments, from 47.6 to 66.5 g kg⁻¹ (Table 3), demonstrated the influence of the environment on the expression of this trait. The mean β -glucan content in 1996 was 21% greater than in 1997. None of the climatic variables measured demonstrated significant effects on mean β -glucan content, likely due to the limited sample of environments tested. The changes in differences among lines across environments is evidence of the genotype-by-environment interaction reported by Peterson et al. (1995), Brunner and Freed (1994), and Welch et al. (1991). To analyze the stability of β -glucan content of lines and checks across environments, the correlation between β -glucan contents measured in different environments was estimated for each pair of environments. All correlation coefficients were significant and ranged from 0.63 to 0.82, suggesting that β -glucan content is moderately stable across environments. The correlation between the β -glucan content of genotypes evaluated at Ames and Nashua averaged across years was 0.86 ($P < 0.01$) and the correlation of β -glucan contents in 1996 and 1997 averaged across locations was 0.67 ($P < 0.01$), indicating that β -glucan contents were more stable across the locations than across the years tested in this study.

To specifically investigate the stability of genotypes with the greatest β -glucan contents, 10 lines with highest mean β -glucan content averaged across environments from each set were checked to see how often they ranked within the top 10 for high β -glucan content within each of the four evaluation environments. As an example, within the four

different evaluation environments, 60 to 70% of the 10 lines with highest overall mean β -glucan contents from set one ranked in the top 10 of 100 entries (Table 3). Averaged across all sets and environments, the overall 10 best lines within sets ranked in the top 10 within environments 61% of the time. Furthermore, since selections were made on the basis of β -glucan content of plants grown in Idaho, while evaluation of response to selection was performed in Iowa, the observed gains in population means demonstrated that β -glucan content was sufficiently stable across environments to permit substantial progress from breeding to be observed across diverse environments.

Components of variance and heritability

The family, family-by-environment, and line within family components of variance were significant in each population except for IABGPI, in which the family variance component was not significantly different from zero (Table 4), perhaps due to the limited sample of families of that population. The genetic components of variance were larger than their respective genotypic-by-environment interaction variances in each population. The environment-by-line within family interaction variance was estimated as the difference between the residual variance, which included the environment-by-line within family interaction variance confounded with the error variance, and the error variance estimated from the repeated checks. Estimates of the environment-by-line within family interaction variance were not significant. It is possible that our estimate of the experimental error variance overestimated the real value of the parameter, leading to an underestimate of the environment-by-line within family interaction variance. Heritability estimates ranged from

0.49 to 0.65 estimated on a $S_{0.1}$ line sample-basis (Table 5). These estimates were similar to the values reported by Kibite and Edney (1998) and Holthaus et al. (1996). Heritability estimated on a line mean-basis ranged from 0.80 to 0.88 and heritability estimated on a family mean-basis ranged from 0.46 to 0.77 (Table 5).

The contrasts σ^2_{family} vs $\sigma^2_{\text{line(family)}}$ for IABG1C0 and σ^2_{family} vs $3\sigma^2_{\text{line(family)}}$ for the IABG1C1, IABG2C0 and IABG2C1 populations were not significant (Table 4), indicating that we could not reject the null hypothesis that additive genetic variance was the only substantial component of the genetic variance. This result agrees with earlier reports that oat β -glucan is a polygenic trait under the control of genes with mainly additive effects (Kibite and Edney, 1998; Holthaus et al., 1996). Assuming that additive genetic variance is the sole genetic component of variance, the estimator of the total genetic variance in a random mated population is equal to the estimator of the genetic variance given by $\sigma^2_{\text{family}} + \sigma^2_{\text{line(family)}}$ (Table 4).

Since genetic variance depends on gene frequency, selection may cause changes in the components of variance (Falconer and Mackay, 1996). We observed reductions of 9.3% and 21.8% in the genetic variance for β -glucan content in IABG1 and IABG2, respectively, after one cycle of selection for greater β -glucan content (Table 3). The phenotypic and genotypic variances of the IABG1 population exhibited similar reductions after selection, so the estimates of heritability on a sample-basis were very similar before and after selection. The phenotypic variance in IABG2 was reduced by approximately half the amount of reduction of the genotypic variance, resulting in a decrease of heritability on a sample-basis from 0.55 to 0.49 (Table 5).

Although the intensity of selection in the IABG2 population was lower than in IABG1 (2.4 % vs 5.5 % of population selected, respectively), the reduction in the genetic variance in IABG2 following selection was nearly double the reduction of the genetic variance of IABG1 (Table 3). A possible explanation is that before selection, the frequency of favorable alleles at loci controlling β -glucan content was greater in IABG2 than in IABG1 and in an interval where small increases in gene frequency cause larger decreases in additive variance (Falconer and Mackay, 1996). The mean β -glucan content of IABG2C1 was highest among populations and its heritability was lowest. Thus, continued selection for greater β -glucan content in this population may result in lower realized gains.

The PI parents (Table 1) were unrelated to the adapted parents of the IABG1 population. Therefore, introduction of PI germplasm was expected to contribute to an increase of the genetic variance when intermated with the selected parental lines of IABG1. Such an increase was observed: IABGPI had a genetic variance 26 % greater than IABG1C1 and 14.5 % greater than IABG1C0 (Table 4). On the other hand, the introduction of this germplasm decreased the mean β -glucan content by 4.6 % relative to IABG1C1 (Table 2).

Predicted responses to selection

The predicted response to selection was 6.8 g kg^{-1} in IABG1 and 3.9 g kg^{-1} in IABG2. Lower gain was expected in IABG2 because the intensity of selection among full-sib families and S_0 lines within full-sib families, 27% and 60%, were lower than the intensity of selection of 2.4% among S_0 lines in IABG1. The realized responses to selection were $5.9 \pm 1.2 \text{ g kg}^{-1}$ in IABG1 and $2.6 \pm 1.1 \text{ g kg}^{-1}$ in IABG2. The observed responses did not differ significantly

from the expected responses. However, the realized responses were consistently lower than predicted. This was likely due to a bias in the heritability estimates, which were based on measurements of a bulk of grain from many plants per line, whereas the actual selections were performed on the basis of individual plants. The error variance of single plant measurements is expected to be larger than that of the samples of grain bulked from many plots. Furthermore, whereas the response to selection conducted in Idaho was evaluated in Iowa, estimates of genotype-by-environment interaction variance were based only on Iowa environments, perhaps leading to overestimation of the effective heritability.

Conclusion

Phenotypic selection of field-grown S_0 plants for greater β -glucan content increased the mean of this trait in the IABG1 and IABG2 populations by 11% and 4%. The intermediate heritability, the predominantly additive inheritance, the significant genetic variability of the trait along, and the availability of instruments to rapidly measure groat β -glucan concentration allowed substantial improvements to be made with single plant phenotypic selection. Furthermore, β -glucan content of improved genotypes was stable across environments, indicating that selections made in only one environment can be expected to result in improvements realized in other environments. The germplasm lines with elevated β -glucan content developed from this program should prove useful as breeding parents for cultivar development programs.

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Table 1. Crosses involving plant introductions of oat that contributed to IABGPI and IABG2C0 populations.

Cross	Pedigree
IA92001	PI361884 (from Romania)//PI412689 (from Turkey)/IL85-6183-1
IA92002	PI412928 (from South Africa)//PI412689 (from Turkey)/IL85-6183-1
IA92003	PI504601 (from Penn. State Univ.)//PI411649 (<i>A. sterilis</i> from Eritrea) /MO07929
IA92004	PI504611 (from Penn. State Univ.)// PI411649 (<i>A. sterilis</i> from Eritrea) /MO07929
IA92005	PI361886 (from Romania)//PI309123 (<i>A. sterilis</i> from Israel)/H87-24
IA92006	PI504593 (from Penn. State Univ.)// PI309123 (<i>A. sterilis</i> from Israel) /H87-24
IA92007	PI502955 (from Iowa State Univ., 25% of parentage is PI298129, <i>A. sterilis</i> from Israel)//PI295903 (<i>A. sterilis</i> from Israel)/IA91539
IA92008	Marion// PI295903 (<i>A. sterilis</i> from Israel)/IA91539
IA92009	PI309598 (<i>A. sterilis</i> from Israel)//Premier
IA92010	PI412418 (<i>A. sterilis</i> from Israel)//Premier

Table 2. Means of groat β -glucan content of the initial and selected generations of the two broad-based oat populations, the wild germplasm donor population, parental lines, and check cultivars averaged across environments.

Population or group	β -glucan content g kg ⁻¹
Check cultivars	55.4 a [†]
Parental lines	54.8 a
IABG1C0	54.0 a
IABG1C1	59.8 b
IABG2C0	63.5 c
IABG2C1	66.1 d
IABGPI	57.1 b

[†] Means followed by the same letter are not significantly different at $P = 0.05$ based on orthogonal contrasts.

The IABG1C1 mean was significantly different from IABGPI mean at $P = 0.08$.

Table 3. β -glucan content and rank of experimental oat lines with greatest mean β -glucan contents across environments and check cultivars from set one within and across each of four Iowa environments.

Population	Line	1996		1997		Average
		Ames	Nashua	Ames	Nashua	
<hr/>						
		g kg ⁻¹				
<hr/>						
IABG2C0	IA94031-6	86.6 (2) [†]	77.6 (6)	53.6 (16)	59.3 (16)	69.3 (1)
IABG2C1	IA95172-1	71.2 (16)	79.0 (5)	57.7 (4)	67.7 (2)	68.9 (2)
IABG2C1	IA95109-2	73.8 (11)	75.7 (9)	60.2 (2)	64.9 (5)	68.6 (3)
IABG2C1	IA95029-3	70.4 (23)	79.6 (4)	58.4 (3)	65.5 (4)	68.5 (4)
IABG2C1	IA95148-3	76.5 (7)	81.2 (1)	55.5 (8)	59.1 (18)	68.1 (5)
IABG2C1	IA95109-3	82.0 (3)	74.7 (11)	53.2 (20)	62.2 (9)	68.0 (6)
IABG2C0	IA94190-10	78.9 (5)	80.8 (2)	54.4 (12)	54.4 (28)	67.9 (7)
IABG1C1	IA93034-2	69.4 (29)	71.4 (22)	61.5 (1)	69.1 (1)	67.8 (8)
IABG2C0	IA94190-1	74.4 (9)	73.9 (24)	57.1 (5)	64.3 (6)	67.4 (9)
IABG1C1	IA93029-6	81.6 (4)	71.8 (21)	55.4 (9)	57.0 (30)	66.5 (10)
Checks	IAN979-5-2 [‡]	72.0 (13)	71.0 (23)	48.6 (42)	65.6 (3)	64.4 (11)
	Starter	64.0 (48)	59.7 (71)	45.6 (56)	55.9 (39)	56.4 (54)
	Hazel	56.0 (78)	56.7 (83)	37.6 (84)	52.6 (51)	50.7 (72)
	Noble	49.6 (85)	60.9 (65)	43.0 (68)	47.0 (71)	50.2 (76)
	Don	47.8 (87)	60.9 (66)	39.0 (81)	45.9 (74)	48.4 (78)
	Ogle	52.5 (82)	57.5 (80)	39.9 (78)	41.8 (81)	48.0 (79)
Mean of all entries		64.9	66.5	47.6	53.7	58.2
LSD [§]	Line vs Line	9.2	9.9	5.8	6.1	3.8
	Line vs Check	8.0	8.5	5.0	5.3	2.9
	Check vs	6.5	7.0	4.1	4.3	1.2
	Check					

[†] Rank of genotypes within parenthesis.

[‡] Considered as a line for pair-wise comparisons.

[§] Least significant difference at the 0.05 probability level.

Table 4. Variance component estimates and their standard deviations for β -glucan content from each of four experimental oat populations.

Source	IABG1C0	IABG1C1	Change	IABG2C0	IABG2C1	Change	IABGPI
	$\text{g}^2 \text{kg}^{-2}$		%	$\text{g}^2 \text{kg}^{-2}$		%	$\text{g}^2 \text{kg}^{-2}$
Family	7.6** (3.1) [†]	10.6** (3.7)	41	12.6** (3.8)	10.3** (3.4)	-19	6.4 (5.7)
Env. x Family	4.8** (1.2)	2.4* (1.1)	-49	6.2** (1.5)	7.5** (1.6)	19	5.0** (1.9)
Line (Family)	7.7** (2.0)	3.2** (1.3)	-59	4.7** (1.5)	3.3** (1.32)	-30	11.0** (4.6)
Residual ‡	7.0** (0.9)	7.2** (1.1)	4	8.3** (1.1)	7.0** (1.0)	-16	4.7* (1.1)
Error §	7.7 (1.0)	7.7 (1.0)		7.7 (1.0)	7.7 (1.0)		7.7 (1.0)
Env. x Line(Fam.)	0	0	0	0.6 (0.5)	0	0	0
σ^2_{ph} ¶	26.8	23.2	-13.4	31.7	27.8	-12	27.0
σ^2_{G} #	15.2	13.8	-9.3	17.4	13.6	-22	17.4
$\sigma^2_{\text{f}} - \sigma^2_{\text{l(f)}}$ ††	-0.1	NA**		NA	NA		NA
$\sigma^2_{\text{f}} - 3\sigma^2_{\text{l(f)}}$	NA	1.1		-1.6	0.3		NA

*, ** Significant component of variance at the 0.05 and 0.01 probability levels, respectively.

† Sampling standard deviations of components of variance estimates within parenthesis.

‡ Residual variance equals $\sigma^2_{\text{env} \times \text{line}(\text{family})} + \sigma^2_{\text{error}}$.

§ Error variance estimated from repeated checks.

¶ Phenotypic variance estimated as: $\sigma^2_{\text{family}} + \sigma^2_{\text{line}(\text{family})} + \sigma^2_{\text{env} \times \text{family}} + \sigma^2_{\text{residual}}$.

Genetic variance estimated as $\sigma^2_{\text{family}} + \sigma^2_{\text{line}(\text{family})}$.

†† σ^2_{f} = Full-sib family variance and $\sigma^2_{\text{l(f)}}$ = $S_{0:1}$ line within family variance.

‡‡ Not applicable (NA).

Table 5. Heritability estimates (and their standard deviations) for β -glucan content within each of five experimental oat populations.

Heritability	IABG1		IABG2		IABGPI
	C0	C1	C0	C1	
$S_{0:1}$ Line sample-basis [†]	0.56 (0.06) [‡]	0.58 (0.08)	0.55 (0.06)	0.49 (0.06)	0.65 (0.13)
$S_{0:1}$ Line mean-basis [§]	0.84 (0.03)	0.85 (0.04)	0.83 (0.03)	0.80 (0.04)	0.88 (0.06)
Full-sib family mean-basis [¶]	0.56 (0.12)	0.77 (0.08)	0.72 (0.08)	0.70 (0.09)	0.46 (0.26)

† Heritability on an $S_{0:1}$ line sample-basis estimated as: $(\sigma^2_{\text{family}} + \sigma^2_{\text{line(family)}}) / (\sigma^2_{\text{family}} + \sigma^2_{\text{line(family)}} + \sigma^2_{\text{env} \times \text{line(family)}} + \sigma^2_{\text{error}})$.

‡ Standard deviations of the heritability estimates within parenthesis.

§ Heritability on an $S_{0:1}$ line mean-basis estimated as: $(\sigma^2_{\text{family}} + \sigma^2_{\text{line(family)}}) / [\sigma^2_{\text{family}} + \sigma^2_{\text{line(family)}} + (\sigma^2_{\text{env} \times \text{family}} + \sigma^2_{\text{env} \times \text{line(family)}} + \sigma^2_{\text{error}}) / 4]$.

¶ Heritability on a full-sib family mean-basis estimated as: $\sigma^2_{\text{family}} / [\sigma^2_{\text{family}} + \sigma^2_{\text{line(family)}} / 2 + \sigma^2_{\text{env} \times \text{family}} / 4 + (\sigma^2_{\text{env} \times \text{line(family)}} + \sigma^2_{\text{error}}) / 8]$.

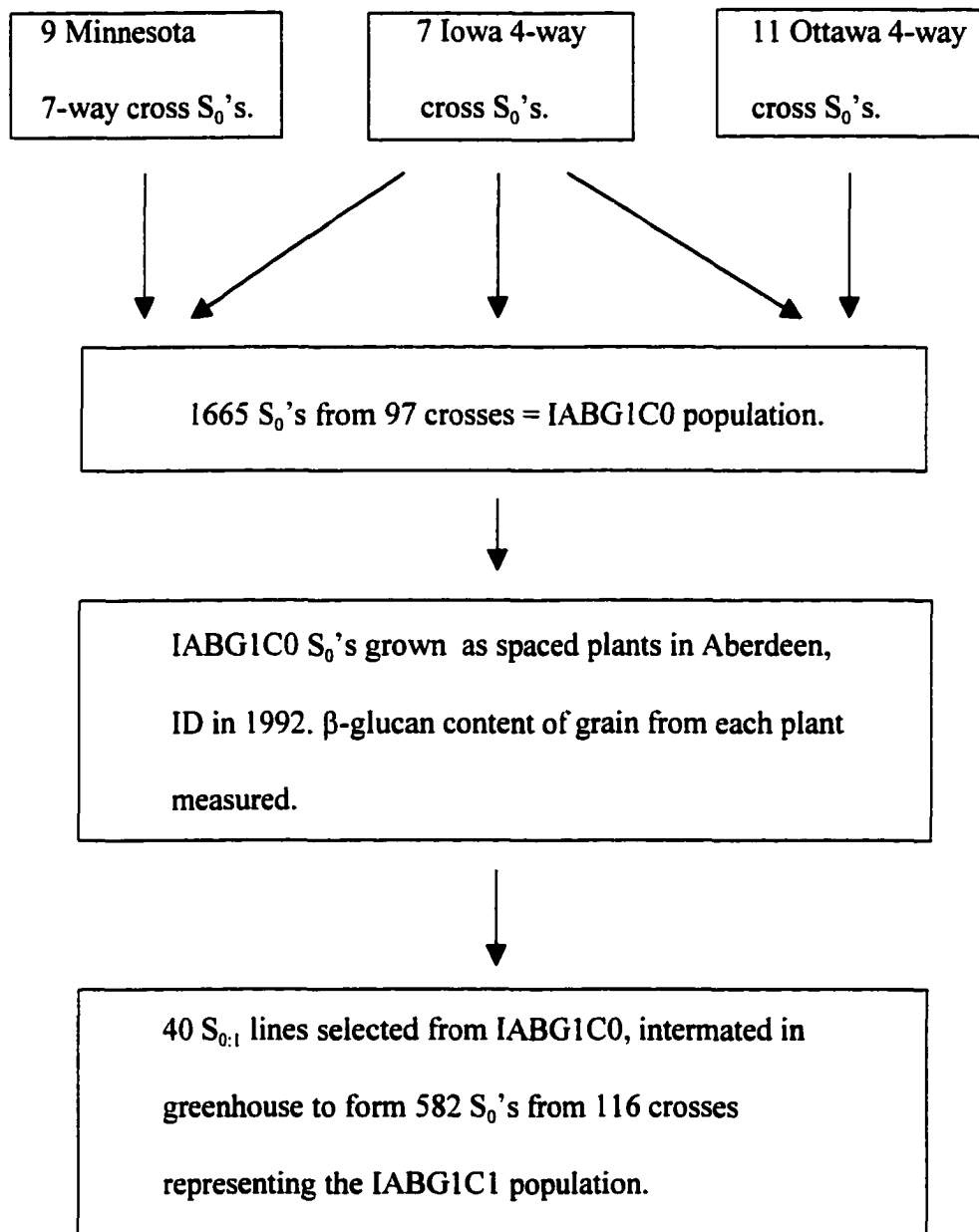


Figure 1. Development of the IABG1C0 and IABG1C1 populations.

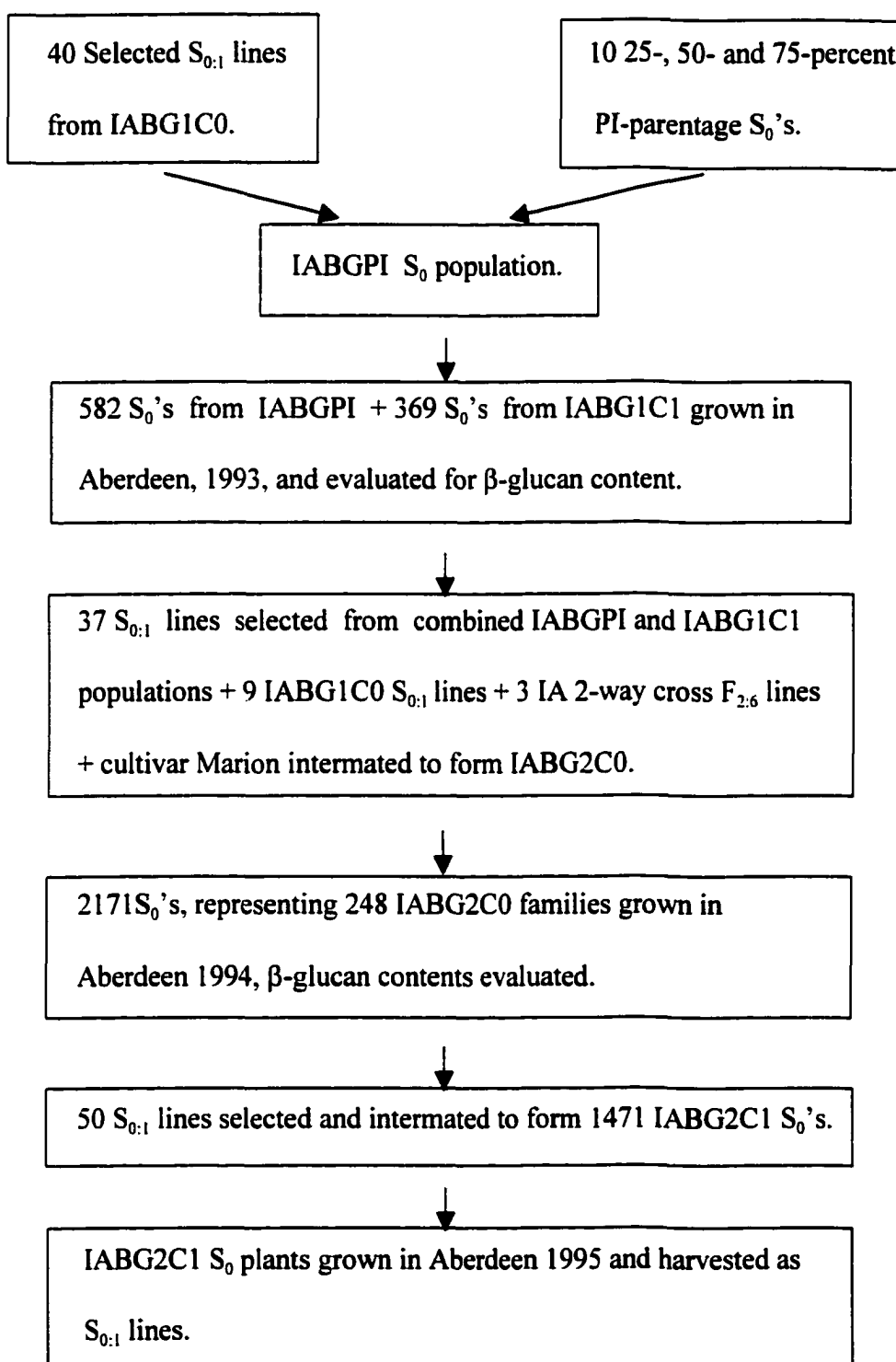


Figure 2. Development of the IABG2C0 and IABG2C1 populations.

CHAPTER 4. CORRELATED RESPONSES TO SELECTION FOR GREATER β - GLUCAN CONTENT IN TWO OAT POPULATIONS

A paper to be submitted to *Crop Science*

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Abstract

Oat (*Avena sativa* L.) β -glucan lowers serum cholesterol in humans. Thus, enhancing its content in oat cultivars for human consumption is desirable. Phenotypic selection for greater β -glucan content has been effective at increasing the β -glucan content in oat grain. The initial (C0) and selected (C1) generations of two broad-based oat populations, IABG1 and IABG2, were evaluated in 1996 and 1997 at two Iowa locations to determine the correlated responses of agronomic and grain quality traits to selection for greater β -glucan content. Mean grain yield, biomass, and test weight were reduced by 19, 17, and 2%, respectively, in one population and not affected in the other. Mean protein content increased by 5% in one population while the mean oil content and heading date did not change. Plant height decreased by 3% in one population only. Correlated responses were generally favorable in terms of human nutritional value of oat grain, but unfavorable for agronomic performance.

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The genotypic variance was not affected for all traits, except for plant height whose genetic variance was increased in IABG2. Selection increased negative genetic correlations between β -glucan content and grain yield, biomass, and oil content in both populations, and between β -glucan content and test weight, heading date, and height in one population. β -glucan yield (the product of β -glucan content and grain yield), had a genetic correlation of 0.92 with grain yield in both base populations and 0.66 and 0.26 with β -glucan content in the two populations. Selection for greater β -glucan yield could be used to improve β -glucan content and grain yield simultaneously.

Introduction

High serum cholesterol level is a major risk factor of premature heart disease in humans (Mayes, 1990; Phillips et al., 1978). The effect of a diet on serum cholesterol is, therefore, a major concern in human nutrition. Oat soluble fiber lowers blood cholesterol levels when consumed in the daily diet, particularly in those individuals with initially high blood cholesterol level (Kurtzweil, 1996; Welch, 1995). The component responsible for lowering serum cholesterol is (1 \rightarrow 3)(1 \rightarrow 4)- β -D-glucan, or β -glucan, a cell wall polysaccharide found in the endosperm and subaleurone layers of cereal seeds (Davidson et al., 1991; Behall et al., 1997). Oat cultivars with greater β -glucan concentrations are desirable for human consumption.

Oat β -glucan content is a polygenic trait controlled by genes with mainly additive effects and no intergenic interaction, with heritability estimates ranging from 0.45 to 0.58

estimated on a single plot basis (Cervantes-Martinez et al., 2000; Kibite and Edney, 1998; Holthaus et al., 1996). Cervantes-Martinez et al. (2000) conducted one cycle of phenotypic selection of individual S_0 plants for greater β -glucan content in two genetically broad-based oat populations. They found that mean β -glucan content increased 5.9 g kg^{-1} and 2.6 g kg^{-1} , and the genetic variance decreased by 9.3% and 21.8% in the two populations, respectively. Ranking of oat lines for β -glucan were generally consistent across environments. These findings indicate that phenotypic selection for greater β -glucan content will be effective to develop cultivars with elevated β -glucan content.

The potential association of oat β -glucan content with agronomic characters and other grain quality traits is important to consider because selection for greater β -glucan content might also change other traits as a correlated response. Correlated responses may cause changes in favorable or unfavorable directions in agronomically important traits when direct selection for a single trait is practiced. For example, Payne et al. (1986) reported that three cycles of recurrent selection for grain yield in spring oats increased grain yield, kernel number, kernel weight, and rate of grain filling, whereas heading date and maturity were delayed. Schipper and Frey (1992) found that five cycles of recurrent selection for greater groat oil content in oat did not affect groat protein content, but four cycles of recurrent selection for greater groat protein increased groat oil content.

Correlated responses to selection depend on the genetic correlation between the selected trait and other traits. Genetic correlations are caused by either or both of pleiotropy, in which the same gene affects different traits, or linkage, when traits are controlled by different genes, but the loci are genetically linked (Falconer and Mackay, 1996). Phenotypic

correlations between traits can be due to genetic or environmental effects or both. β -glucan content is not strongly correlated with grain yield (Kibite and Edney, 1998; Holthaus et al., 1996). However, Holthaus et al. (1996) reported a low positive phenotypic correlation, Kibite and Edney (1998) found a low negative phenotypic correlation, and Peterson et al. (1995) reported both low positive and negative correlations of β -glucan with grain yield. Phenotypic correlations of β -glucan with yield can also change from positive to negative depending on the environment (Brunner and Freed, 1994). β -glucan content has also exhibited positive or nonsignificant correlations with test weight (Peterson et al., 1995), protein (Brunner and Freed, 1994) and groat percentage (Holthaus et al., 1996). However, Saastamoinen et al. (1992) reported relatively high negative correlations of β -glucan concentration with protein content. β -Glucan concentration has been found to be negatively correlated with oil content (Kibite and Edney, 1998; Welch and Lloyd, 1989). Negative and nonsignificant correlations of β -glucan content and groat weight have been found (Holthaus et al., 1996). Brunner and Freed (1994) attributed the negative correlation of β -glucan and groat weight to a greater ratio of cell wall to cell content in small groats. Groat β -glucan content tends to show no association with heading date and plant height (Holthaus et al., 1996; Welch and Lloyd, 1989), although some negative correlations have been reported (Peterson et al., 1995).

Because selection for greater β -glucan content is designed to improve the effect of oat grain on human health, its effect on other components that affect the dietary quality of the grain, such as protein and oil, should be investigated. Oat grain protein has a well-balanced amino acid composition and greater digestibility than legume protein (Barnes, 1982).

Increases in groat protein content of oats improve the nutritional value of the crop. On the other hand, increases in groat oil content would be unfavorable for human diets, because oat grain is used to contribute to a low fat and high soluble fiber diet (Holland, 1997).

Correlated response can be exploited to increase the expression of a primary trait if selection for a secondary trait produces greater genetic gain in the primary trait than direct selection (Hallauer and Miranda, 1988). Theoretically, this is possible when the product of the genetic additive correlation and the square root of the narrow sense heritability of the second trait is larger than the square root of the heritability of the main trait of interest (Falconer and Mackay, 1996). For example, Johnson et al. (1983) compared direct selection for increasing grain yield to indirect selection using vegetative growth rate on F₂-derived oat lines. They found that indirect selection via vegetative growth rate gave a greater increase in grain yield than direct selection for grain yield. Helsel (1985) also reported that indirect selection of biomass plus harvest index was more effective for improving oat grain yield than direct selection for grain yield.

The objectives of this study were 1) to estimate the correlated responses to selection of individual S₀ plants for high β -glucan in two oat populations, 2) to estimate changes in genetic variation and heritability of unselected traits in these populations, and 3) to estimate genetic covariances and correlations between β -glucan content and grain quality and agronomic traits in these populations.

Materials and Methods

The development of the oat populations was described in detail by Cervantes-Martinez et al. (2000). The original population was developed by the intermating of oat

breeding lines and commercial cultivars chosen for their high β -glucan content or good agronomic characteristics. The S_0 seed of the base population for selection, IABG1C0, was obtained from crosses involving primarily cultivars and experimental lines adapted to Iowa, Minnesota, or Ottawa, Canada, and chosen for their high β -glucan content. Selection for high β -glucan content was practiced among S_0 plants of IABG1C0 grown in Aberdeen, ID, in 1992. The S_0 seed of the IABG1C1 population was developed from crosses among 40 parental $S_{0:1}$ lines selected from IABG1C0.

A second base population (IABG2C0) was developed intermating the lines from IABG1C1 with highest β -glucan content and lines from the IABGPI population, which had from 12 to 37 % plant introduction parentage. Selection for greater β -glucan content was practiced among S_0 plants from IABG2C0 grown in Aberdeen, ID, in 1994. A single line with highest β -glucan content within each of the 50 families with highest mean β -glucan contents was selected. Fifty $S_{0:1}$ lines were selected from IABG2C0 and intermated in the greenhouse to produce S_0 seed of the IABG2C1 population. IABG2C1 S_0 plants were grown without selections in Aberdeen, ID, in 1995 to develop $S_{0:1}$ lines.

The IABG1C0, IABG1C1, IABG2C0, IABG2C1 and IABGPI populations were evaluated in a field experiment in 1996 and 1997. Fifty full-sib families from each of the IABG1C0, IABG2C0, IABG2C1 populations, and 33 and 17 full-sib families from the IABG1C1 and IABGPI populations, respectively, were randomly chosen for evaluation. $S_{0:1}$ lines derived from the same cross represented a full-sib family. Two $S_{0:1}$ lines were randomly chosen from each full-sib family for evaluation, resulting in a total of 400 experimental $S_{0:1}$ lines in the experiment. The experimental design was a sets within

replications design, in which each set received two $S_{0:1}$ lines from each of 10 full-sib families from each of the IABG1C0, IABG2C0, IABG2C1 populations, two $S_{0:1}$ families from each of 4 to 10 full sib families of the IABG1C1 population, and two $S_{0:1}$ families from each of zero to six full-sib families of the IABGPI population to make a total of 40 full-sib families. Seven commercial oat cultivars were included in each set in duplicate. Each set also included five of the original parental lines, which were assigned to sets at random, and the high β -glucan experimental line, IAN979-5-2. Each set of 100 entries was arranged as a 10 x 10 square lattice with two replications at each environment. The experiment was grown at the Agronomy and Agricultural Engineering Field Research Center near Ames and the Northeast Research Center near Nashua, IA in both years. The soil types were a Nicollet loam soil (fine-loamy, mixed, mesic Aquic Hapludoll) at Ames and a Readlyn loam soil (fine-loamy, mixed, mesic Aquic Hapludoll) at Nashua. Field plots were hills of 20 seeds spaced 0.3 m apart in perpendicular directions. Two rows of hills of a common check cultivar surrounded each set to provide competition to peripheral plots. Field experimental procedures were described by Cervantes-Martinez et al. (2000).

Heading date was recorded as the date when 50% of panicles in a plot were fully emerged. Plant height was measured as the distance from the ground surface to panicle tips. Heading date and plant height were measured in Ames in both years. Total above-ground biomass and grain yield were measured on each plot. In order to have sufficient seed for spectrophotometry and chemical analysis, the grain from both replications of an entry within a location was bulked together and mixed thoroughly. Test weight was measured on each bulk of grain. Grain samples were then dehulled using an air pressure dehuller (Codema brand model LH 5095) to obtain approximately 8 g of groats.

The β -glucan, protein and oil contents of each goat sample were estimated with standard near-infrared reflectance spectrophotometer (NIRS) equipment (Pacific Scientific Model 6250). The β -glucan, protein and oil values for each sample were the mean of three measurements. β -glucan contents of 92 samples from the 1996 evaluation and 95 samples from the 1997 evaluation, representing approximately 10% of the total number of samples from each year's evaluation were measured with the automated flow injection analysis (FIA), as described by Lim et al. (1992), to calibrate the prediction equation for β -glucan content for each year evaluation. Protein contents of 52 samples (3% of the total number of samples) were measured using the Kjeldahl procedure (Bremner and Breitenbeck, 1983) to calibrate the prediction equation for protein content. Oil contents of 74 samples from the 1996 evaluation and 99 samples for the 1997 evaluation (representing 8 and 11% of the total number of samples from each year, respectively) were determined by Nuclear Magnetic Resonance (Conway and Earle, 1963) performed at the University of Illinois to calibrate the prediction equation for oil content for each year evaluation. The calibration samples were selected on the basis of spectral features to represent the spectral variability of the whole set of samples. The prediction equations for each year of evaluation were developed using modified partial least squares (Benson, 1986).

Statistical analysis

To compare population means, each trait was analyzed separately considering the overall mean and populations as fixed effect factors and all other factors as random and using PROC MIXED of SAS (Littell et al., 1996). Significance of correlated responses to selection for greater β -glucan content were tested using contrasts between the IABG1C0 and

IABG1C1 populations means and between the IABG2C0 and IABG2C1 populations means. Heading date, plant height, grain yield, and biomass were measured on individual plots, so best linear unbiased predictors (BLUPs) of entries within environments were estimated to remove the effects of incomplete blocks. The subsequent analyses were performed on the basis of each entry's BLUP within each environment. Test weight and groat β -glucan, protein, and oil contents were measured on a sample of seed bulked over replicate plots at each location. Therefore, the analyses for these traits were performed on the basis of each entry's bulk sample within each environment.

The components of variance were estimated for each population (IABG1C0, IABG1C1, IABG2C0, IABG2C1, IABGPI) separately with the restricted maximum likelihood (REML) method (Searle, 1971) of SAS PROC MIXED (Littell et al., 1996), considering all effects except the overall mean random. Check entries were not included in this analysis. The residual variance of the analysis for all traits included the environment-by-line within family interaction variance confounded with the error variance. To partition these two components of variance for heading date, plant height, grain yield, and biomass, the error variance was estimated as the pooled variance of the experimental error of the overall analysis of variance performed on plot measurements of all entries. The estimates of the error variances for test weight, and groat β -glucan, protein and oil content were obtained by analyzing the seven check entries (commercial cultivars) duplicated within each set. The error variance was estimated as a pooled variance of repeated checks within sets and environments. In both cases, a contrast of the residual variance vs the error variance was performed assuming asymptotic normality (Self and Liang, 1987; Searle, 1971).

Significance tests of the other components of variance were performed with a chi-square test

of the difference between the -2 REML log-likelihood of the complete model and the model without the component of variance in question (Self and Liang, 1987; Littell et al., 1996).

The genetic expectancies of family and $S_{0:1}$ line within family variance components of the IABG1C0 population can be written as follows: $\sigma^2_{\text{family}} = (1/2)\sigma^2_A + (1/32)\sigma^2_D + (1/2)D_1 + (1/16)D_2 + (1/4)\sigma^2_{AA} + (1/32)\sigma^2_{AD} + (1/256)\sigma^2_{DD}$ and $\sigma^2_{\text{line(family)}} = (1/2)\sigma^2_A + (3/16)\sigma^2_D + (1/2)D_1 + (1/16)D_2 + (3/4)\sigma^2_{AA} + (7/32)\sigma^2_{AD} + (15/256)\sigma^2_{DD}$, where σ^2_A is the additive, σ^2_D is the dominance variance, D_1 is the covariance between additive effects and homozygous dominant effects and D_2 is the variance of homozygous dominant effects, and σ^2_{AA} , σ^2_{AD} and σ^2_{DD} are the additive x additive, additive x dominant and dominant x dominant epistatic variances, respectively (Cervantes-Martinez et al., 2000; Nyquist, 1991; Cockerham, 1983). The variance components of family and $S_{0:1}$ line within variance of the IABG1C1, IABG2C0, and IABG2C1 populations are: $\sigma^2_{\text{family}} = (3/4)\sigma^2_A + (9/64)\sigma^2_D + (3/4)D_1 + (3/32)D_2 + (9/16)\sigma^2_{AA} + (27/256)\sigma^2_{AD} + (81/4096)\sigma^2_{DD}$ and $\sigma^2_{\text{line(family)}} = (1/4)\sigma^2_A + (7/64)\sigma^2_D + (1/4)D_1 + (1/32)D_2 + (7/16)\sigma^2_{AA} + (37/256)\sigma^2_{AD} + (175/4096)\sigma^2_{DD}$ (Cervantes-Martinez et al. 2000).

When genetic variance is entirely additive, the difference between the genetic components of variance fits the following equalities: $\sigma^2_{\text{family}} - \sigma^2_{\text{line(family)}} = 0$ for IABG1C0 and $\sigma^2_{\text{family}} - 3\sigma^2_{\text{line(family)}} = 0$ for the IABG1C1, IABG2C0, and IABG2C1 populations. These equations were tested with an asymptotic Z test.

The estimates of phenotypic variance on a plot-basis for height, heading date, biomass, and grain yield were obtained as the sum of the variance components due to family, $S_{0:1}$ lines within families, family-by-environment interaction, environment-by-line within

family interaction, and experimental error. The phenotypic variances on a bulk sample-basis for test weight, β -glucan, and protein and oil content were obtained as the sum of the variance components due to family, $S_{0:1}$ lines within families, family-by-environment interaction, environment-by-line within family interaction, and experimental error. The phenotypic variance on a line mean-basis was estimated for height and heading date as:

$$\hat{\sigma}_{\bar{p}}^2 = \hat{\sigma}_{family}^2 + \hat{\sigma}_{line(family)}^2 + (\hat{\sigma}_{env \times family}^2 + \hat{\sigma}_{env \times line(family)}^2) / 2 + (\hat{\sigma}_{error}^2) / 4$$

for yield and biomass as:

$$\hat{\sigma}_{\bar{p}}^2 = \hat{\sigma}_{family}^2 + \hat{\sigma}_{line(family)}^2 + (\hat{\sigma}_{env \times family}^2 + \hat{\sigma}_{env \times line(family)}^2) / 4 + (\hat{\sigma}_{error}^2) / 8$$

and for test weight, and β -glucan, protein and oil content as:

$$\hat{\sigma}_{\bar{p}}^2 = \hat{\sigma}_{family}^2 + \hat{\sigma}_{line(family)}^2 + (\hat{\sigma}_{env \times family}^2 + \hat{\sigma}_{env \times line(family)}^2 + \hat{\sigma}_{error}^2) / 4.$$

The phenotypic variance on a family mean-basis was estimated for height and heading date as:

$$\hat{\sigma}_{\bar{p}_{family}}^2 = \hat{\sigma}_{family}^2 + (\hat{\sigma}_{line(family)}^2 + \hat{\sigma}_{env \times family}^2) / 2 + (\hat{\sigma}_{env \times line(family)}^2) / 4 + (\hat{\sigma}_{error}^2) / 8$$

this was estimated for yield and biomass as:

$$\hat{\sigma}_{\bar{p}_{family}}^2 = \hat{\sigma}_{family}^2 + \hat{\sigma}_{line(family)}^2 / 2 + \hat{\sigma}_{env \times family}^2 / 4 + (\hat{\sigma}_{env \times line(family)}^2) / 8 + (\hat{\sigma}_{error}^2) / 16$$

and for test weight, β -glucan, protein and oil content as:

$$\hat{\sigma}_{\bar{p}_{family}}^2 = \hat{\sigma}_{family}^2 + \hat{\sigma}_{line(family)}^2 / 2 + \hat{\sigma}_{env \times family}^2 / 4 + (\hat{\sigma}_{env \times line(family)}^2 + \hat{\sigma}_{error}^2) / 8.$$

Heritabilities on a plot-basis or sample-basis, on a line mean-basis, or on a family mean-basis were estimated as:

$$H^2 = (\hat{\sigma}_{family}^2 + \hat{\sigma}_{line(family)}^2) / \hat{\sigma}_P^2, \quad H^2 = (\hat{\sigma}_{family}^2 + \hat{\sigma}_{line(family)}^2) / \hat{\sigma}_{\bar{P}}^2 \quad \text{and} \quad H^2 = \hat{\sigma}_{family}^2 / \hat{\sigma}_{\bar{P}_{family}}^2,$$

respectively.

The analysis of covariance was performed ignoring the family structure for simplicity. The mean products of environments, lines, and line-by-environment interaction confounded with experimental error were obtained separately for each population. The analyses were performed for each population with the multivariate analysis of variance (MANOVA) option of SAS Proc GLM (SAS Institute, Inc., 1989). The components of variance and covariance were estimated with the method of moments (Mode and Robinson, 1959). The genetic covariance between the traits W and Z was estimated as the covariance component due to lines. The phenotypic covariance was estimated on a sample-basis as:

$$\hat{\sigma}_{P_{WZ}} = \hat{\sigma}_{line_{WZ}} + \hat{\sigma}_{residual_{WZ}}, \quad \text{where } \hat{\sigma}_{line_{WZ}} \text{ is the covariance due to lines and } \hat{\sigma}_{residual_{WZ}} \text{ is the}$$

residual covariance due to environment-by-line interaction confounded with the experimental error covariance.

The phenotypic covariances of β -glucan content with height and heading date on a line mean-basis were estimated as:

$$\hat{\sigma}_{\bar{P}_{WZ}} = \hat{\sigma}_{line_{WZ}} + (\hat{\sigma}_{residual_{WZ}} / 2),$$

and the phenotypic covariances of β -glucan content with yield, biomass, test weight, and protein and oil content were estimated as:

$$\hat{\sigma}_{\bar{p}_{WZ}} = \hat{\sigma}_{line_{WZ}} + (\hat{\sigma}_{residual_{WZ}} / 4),$$

The genetic correlation and phenotypic correlations on a sample-basis and on a line mean-basis between the traits W and Z were obtained as:

$$r_G = \hat{\sigma}_{line_{WZ}} / \sqrt{\hat{\sigma}_{line_W}^2 \hat{\sigma}_{line_Z}^2}, \quad r_P = \hat{\sigma}_{p_{WZ}} / \sqrt{\hat{\sigma}_{p_W}^2 \hat{\sigma}_{p_Z}^2} \quad \text{and} \quad r_{\bar{p}} = \hat{\sigma}_{\bar{p}_{WZ}} / \sqrt{\hat{\sigma}_{\bar{p}_W}^2 \hat{\sigma}_{\bar{p}_Z}^2}, \quad \text{respectively,}$$

where : $\hat{\sigma}_{line_W}$ and $\hat{\sigma}_{line_Z}$ are the variance components due to lines, $\hat{\sigma}_{p_W}^2$ and $\hat{\sigma}_{p_Z}^2$ are the phenotypic variances estimated on a sample - basis, and $\hat{\sigma}_{\bar{p}_W}^2$ and $\hat{\sigma}_{\bar{p}_Z}^2$ are the phenotypic variances estimated on a line mean-basis for the traits W and Z, respectively. Approximate sampling standard errors of the correlation estimates were obtained with the formulas given by Mode and Robinson (1959).

The predicted correlated responses to selection for greater β -glucan content for IABG1 and IABG2 were obtained with the formula $CR_Y = i h_{BG} h_Y r_G \sigma_{p_Y}$, where h_{BG} is the square root of the heritability of β -glucan content, h_Y is the square root of the heritability of trait Y, r_G is the genetic correlation between β -glucan content and trait Y, and σ_{p_Y} is the phenotypic standard deviation of trait Y (Falconer and Mackay, 1996). Heritability on a sample-basis was used to obtain the predicted correlated responses to selection for IABG1. In the case of the IABG2 population, the total predicted correlated response was obtained as the sum of the correlated response to selection among full-sib families and the correlated response to selection of S_0 lines within full-sib families. On average, each full-sib family consisted of three S_0 lines when selection was performed. The heritabilities among and within full-sib families were estimated as:

$$H^2 = \hat{\sigma}_{family}^2 / [\hat{\sigma}_{family}^2 + \hat{\sigma}_{line(family)}^2 / 3 + \hat{\sigma}_{env \times family}^2 + (\hat{\sigma}_{env \times line(family)}^2 + \hat{\sigma}_{error}^2) / 3] \text{ and}$$

$$H^2 = \hat{\sigma}_{line(family)}^2 / (\hat{\sigma}_{line(family)}^2 + \hat{\sigma}_{env \times line(family)}^2 + \hat{\sigma}_{error}^2), \text{ respectively,}$$

The genetic correlations among and within full sib families were estimated as:

$$r_G = \hat{\sigma}_{family_{WZ}} / \sqrt{\hat{\sigma}_{family_W}^2 \hat{\sigma}_{family_Z}^2} \text{ and } r_G = \hat{\sigma}_{line(family)_{WZ}} / \sqrt{\hat{\sigma}_{line(family)_W}^2 \hat{\sigma}_{line(family)_Z}^2},$$

respectively. Heritabilities, genetic correlations, and phenotypic standard deviations were estimated from the evaluation experiments in 1996 and 1997, while the intensity of selection was calculated from the original selection trails.

Results and Discussion

Validation of prediction equations

The prediction equations for β -glucan content had coefficients of determination (R^2) of 0.76 for the 1996 evaluation and 0.80 for 1997, with standard errors of calibration (SEC) of 4.7 g kg⁻¹ and 3.8 g kg⁻¹, respectively (Cervantes-Martinez et al., 2000). The R^2 of the prediction equation for protein content was 0.95 with a SEC of 5.3 g kg⁻¹. The R^2 of the prediction equation for oil content was 0.92 for the 1996 evaluation and 0.90 for 1997. The SEC was 2.1 g kg⁻¹ for 1996 and 2.7 g kg⁻¹ for 1997. Even with larger sample sizes used for calibration, our prediction equations for β -glucan content were less precise than those for protein or oil content. These results indicate that the oat β -glucan content is more difficult to determine than protein and oil content via NIRS. Increasing sample sizes (to more than 10%) for the calibration equation for β -glucan content may be required to improve its reliability.

Correlated responses to selection

The original base population for selection, IABG1C0, had mean agronomic and grain quality traits similar to the commercial cultivars used as checks (Don, Marion, Hazel, Premier, Ogle, Starter, and Noble), except that mean plant height of IABG1C0 was greater than the checks (Table 1). This suggests that the original population IABG1C0 had good agronomic characteristics before selection was made. The IABG1C0 population had greater mean grain yield and biomass and lower mean protein content than its parental lines. The IABG2C0 population had lower mean grain yield, biomass, test weight and oil content, and greater protein content, indicating that the original IABG2C0 population had good grain quality characteristics, but lower performance in agronomic traits before selection was made.

One cycle of selection for greater β -glucan content did not change the mean grain yield, biomass, or test weight in IABG1, but in IABG2 resulted in significant decreases in mean grain yield of 62 g m^{-2} , in biomass of 158 g m^{-2} , and in test weight of 10 kg m^{-3} (Table 1). Mean protein content increased by 9 g kg^{-1} and mean plant height decreased by 3 cm after one cycle of selection in IABG1. They did not change in IABG2. Mean oil content and heading date remained unchanged in both populations.

Lines with highest β -glucan content across environments had a tendency to show lower grain yield and biomass and greater protein content, whereas no pattern was observed for test weight, oil content, heading date, and plant height (Table 2). However, some individual lines with greater β -glucan content and comparable values for agronomic and grain quality traits to the commercial cultivars used as checks were observed in each set. For example, IA94190-1, and IA94190-10, lines with high β -glucan content and similar grain

yield to the best check cultivars, and with good performance in general for biomass, test weight, and protein and oil content, heading date and height, were identified in set one (Table 2). Similar results were observed in the other sets, suggesting that it may be possible to identify lines with superior β -glucan content, grain quality, and agronomic performance from these populations to develop cultivars. Further agronomic evaluation, for example in larger plots more suitable for yield and lodging evaluation, and agronomic evaluation under natural infestation of crown rust (*Puccinia coronata* [Corda.]) will be required to verify the potential of experimental lines to be cultivars. Furthermore, selection and purification within the best lines would be required to develop pure-line cultivars directly from these populations.

Genetic variances and heritabilities

The full-sib family and $S_{0:1}$ line within full-sib family variances were significant for the IABG1C0, IABG1C1, IABG2C0, and IABG2C1 populations for all traits measured, except for the family variance of test weight and heading date in IABG1C0 and the line within family variance for test weight in IABG1C1 (Table 3). The environment-by-family interaction variance was not significant for grain yield, test weight, or height in the four populations, except for test weight in IABG2C0.

The family variance was larger than the environment-by-family interaction variance for all traits in IABG1 and IABG2, except for biomass and test weight in IABG1C0. The environment-by-line within family interaction variance was estimated as the difference of the residual variance and the error variance for all traits. Error variance for heading date, plant height, grain yield, and biomass was estimated as the pooled experimental error variance of the overall analysis on plot measurements. The environment-by-line within family

interaction variance was not significant for these traits in all populations. For test weight and protein and oil contents, the error variance was estimated as a pooled variance of repeated checks within sets and environments. The environment-by-line within family interaction variance was significant for test weight and oil content in IABG1 and IABG2, except for oil content in IABG1C1, but for protein content was significant only in IABG1C0.

The contrasts of σ^2_{family} vs $3\sigma^2_{\text{line(family)}}$ for IABG1C1, IABG2C0 and IABG2C1, and σ^2_{family} vs $\sigma^2_{\text{line(family)}}$ for IABG1C0 for grain yield, biomass, and protein content were generally large but not significant (Table 3); therefore we could not reject the hypothesis that additive variance is the only component of the genetic variance for these traits. Large additive genetic variance does not imply lack of nonadditive genetic effects. Furthermore, the large sampling variances of the estimates of components of variance reduced the power of the test to detect nonadditive components of variance. Nonadditive genetic variances were significant only for test weight and heading date in IABG1C0 (Table 3). These findings agree with those of Pixley and Frey (1991), who reported that test weight, heading date, and plant height are controlled by genes with predominantly additive effects, and with those of Brown et al. (1974), who reported mainly additive genetic inheritance for oil content.

The changes in genetic variance from IABG1C0 to IABG1C1 and from IABG2C0 to IABG2C1 were estimated to determine the effect of selection for greater β -glucan content on the genetic variability of other traits. The phenotypic and the genotypic variances for grain yield, biomass, test weight, and protein and oil content did not significantly change in IABG1 and IABG2 following selection (Table 4). The phenotypic variance decreased for plant height in IABG1, and increased for heading date in IABG1 and height in IABG2. The genotypic variance significantly increased only for plant height in IABG2.

The heritability estimated on a $S_{0:1}$ plot-basis ranged from 0.33 to 0.50 for grain yield, from 0.21 to 0.39 for biomass, from 0.46 to 0.61 for heading date, and from 0.39 to 0.76 for plant height. The heritability estimated on a $S_{0:1}$ sample-basis ranged from 0.30 to 0.61 for test weight, from 0.62 to 0.82 and from 0.74 to 0.90 for protein and oil content, respectively (Table 5). These estimates are lower than the heritability on a plot-basis estimates reported for grain yield, biomass, heading date, and plant height by Hoi et al. (1999), and comparable to the heritability on a line mean basis-estimates reported for yield and test weight by Klein et al. (1993) and for oil content by Schipper and Frey (1991). A possible explanation for this could be the low genotype-by-environment interaction variance shown for all traits in this study. Changes in heritabilities for grain yield, biomass, test weight, and protein and oil content after one cycle of selection for greater β -glucan were generally small in both populations because no significant changes in phenotypic and genotypic variances were observed for these traits (Table 5).

Introduction of unadapted PI parents contributed to an increase of the genetic variance of β -glucan content when intermated with the parents of IABG1C1 to form IABG2C0 (Cervantes-Martinez et al., 2000). The IABGPI population crosses also resulted in a significant increase in the genetic variance of plant height in IABG2C0. On the other hand, introduction of the IABGPI germplasm resulted in a nearly significant ($P = 0.06$) reduction in the genetic variance for protein content of 47%, indicating that the PI germplasm contributed few unique alleles for this trait. Mean test weight was reduced by 5%, while mean oil content increased by 9%. No change was observed in the means of grain yield, biomass, protein content, or heading date (Table 1).

In summary, protein content consistently exhibited the most favorable correlated responses to selection for greater β -glucan content. Mean protein content increased following selection in IABG1 and remained unchanged in IABG2, while its heritability increased in both populations. The increase in heritability may allow greater response to direct selection for greater protein content in these selected populations. On the other hand, unfavorable responses were observed for grain yield, biomass, and test weight whose means were reduced following selection in IABG2. For these traits, it is likely that the frequency of favorable alleles was reduced and response to direct selection to reverse the unfavorable responses in these traits will be reduced (McFerson and Frey, 1992). Selection for greater β -glucan content did not affect the genetic variance for grain yield, biomass, test weight, protein and oil content, or heading date in either population, or plant height in IABG1. Only the genetic variance of plant height increased in IABG2 following selection for greater β -glucan content.

Genotypic and phenotypic correlations

In general, β -glucan content exhibited low negative genetic correlations with grain yield, biomass, test weight, and oil content in IABG1 and IABG2, except in IABG1C0, in which its genetic correlations with grain yield and biomass were positive (Table 6). β -glucan content was positively genetically correlated with protein content in IABG1 and IABG2. Heading and height showed low negative genetic correlation with β -glucan content in IABG1 and low positive correlation in IABG2.

Selection for greater β -glucan content generally resulted in unfavorable changes in genetic correlations between β -glucan content and other traits. Phenotypic selection for

greater β -glucan content caused changes toward larger negative genetic correlations of this trait with yield, biomass, and oil content in IABG1 and IABG2, with test weight in IABG2, and with heading and height in IABG1. The positive genetic correlations of β -glucan with protein content in IABG1 and with height in IABG2 were decreased followed selection. Only the positive genetic correlations of protein content and heading with β -glucan content in the IABG2 population increased following selection (Table 6). Introduction of germplasm from the PI parents reduced the negative effect of selection on the genetic correlation of β -glucan content with grain yield, biomass, test weight, heading date, and height when intermated with the selected parents of IABG1.

Phenotypic correlations on a sample-basis of β -glucan content with agronomic and grain quality traits were generally lower than the corresponding genotypic correlations (Table 6). The estimates of the phenotypic correlation on a sample-basis of β -glucan content with yield, protein and oil content, heading, and plant height obtained in this study were lower than the values reported by other authors (Kibite and Edney, 1998; Holthaus et al., 1996; Peterson et al., 1995; Brunner and Freed, 1994), probably because we estimated the phenotypic correlation directly from the components of variance and covariance, rather than from total variances and covariance. Phenotypic correlations estimated by the latter method are biased.

Predicted correlated response to selection

The predicted correlated responses for grain yield, biomass, test weight, protein and oil content, heading, and height were 38 g m^{-2} , 35 gm^{-2} , -5 kg m^{-3} , 5 g kg^{-1} , -1 g kg^{-1} , 0 d and

-1 cm in IABG1, respectively, and -11 g m^{-2} , -35 g m^{-2} , -2 kg m^{-3} , 0 g kg^{-1} , -1 g kg^{-1} , 0 d and 1 cm in IABG2, respectively. The realized correlated response for yield, biomass, test weight, protein and oil content, heading, and height were 20 g m^{-2} , 4 g m^{-2} , 0 kg m^{-3} , 9 g kg^{-1} , -1 g kg^{-1} , -2 d and -3 cm in IABG1, respectively, and -62 g m^{-2} , -158 g m^{-2} , -10 kg m^{-3} , 0 g kg^{-1} , 1 g kg^{-1} , 1 d and 0 cm in IABG2, respectively (Table 1). Realized responses did not differ significantly from observed responses, except for yield and biomass in IABG2, whose predicted correlated responses were significantly lower than their realized correlated response.

This discrepancy could be due to genotype-by-environment interaction for yield and biomass between the selection environment, Aberdeen 1994, and the evaluation environments, Iowa 1996 and 1997, or it could be due to over-estimating the predicted responses by using heritability on a plot-basis, whereas selections were performed on a single plant-basis. In general, the predicted correlated responses fit the realized ones, indicating that the heritabilities and genetic correlations estimations obtained in this study were good approximations of the true values.

The product of the genetic correlation with the square root of the heritability on a sample-basis of traits that were positively associated in some population with β -glucan content was obtained and compared with the heritability of β -glucan content on a sample-basis to determine if indirect selection would be more effective to increase β -glucan content than direct selection. In all cases this product was lower than the square root of the heritability of β -glucan content on a sample-basis, indicating that direct selection for high β -glucan content is predicted to be more effective at increasing β -glucan content than any

indirect selection. Selection for greater groat β -glucan content also increased negative genetic correlations of this trait with grain yield to $r = -0.25$ in IABG1 and to $r = -0.49$ in IABG2, and decreased the mean yield in IABG2 by 19%, resulting in a 15% reduction in the yield of β -glucan per unit land area, assuming that the groat percentage did not change.

Selection for greater β -glucan yield (the product of groat yield and groat β -glucan content) may be a simple and effective method to simultaneously improve both grain yield and β -glucan content. Previous research on protein content and grain yield in oat suggests that selection for yield of chemical components of grain should be effective. For example, Kuenzel and Frey (1985) reported that protein content and grain yield in oat F_2 -derived lines from 27 matings had a phenotypic correlation of -0.33, while protein yield, obtained as the product of protein content and grain yield, had a phenotypic correlation of -0.09 with protein content and 0.98 with grain yield. Moser and Frey (1994) demonstrated that recurrent selection in oat for greater protein yield was effective at increasing protein yield *per se*, as well as both grain yield and protein content.

β -Glucan yield was estimated assuming a constant groat percentage for all genotypes. This assumption is supported by the general lack of correlation between β -glucan content and groat percentage (Holthaus et al., 1996). The genotypic correlations of β -glucan yield with grain yield and β -glucan content were 0.92 and 0.66, respectively, in IABG1C0 and 0.92 and 0.26, respectively, in IABG2C0. These values suggest that selection for β -glucan yield would allow the improvement of β -glucan content with no decrease in grain yield.

Conclusion

Phenotypic selection of individual S_1 plants for greater groat β -glucan content increased the expression of this trait by 11% in IABG1 and 4% in IABG2 (Cervantes-Martinez et al., 2000). However, it reduced the mean grain yield, biomass, and test weight by 19, 17, and 2%, respectively, in IABG2. The genetic variances of grain quality and agronomic traits were generally not affected. Unfavorable increases in the magnitude of the negative genotypic correlations between β -glucan content and grain yield, biomass, and test weight were observed following selection for greater β -glucan content, and this likely contributed to the unfavorable correlated changes in the IABG2 population mean. Strategies for selecting agronomic traits simultaneously with β -glucan content should be implemented. Selection for greater β -glucan yield is a possibility to improve β -glucan content without decreasing grain yield.

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Table 1. Population means of five experimental oat populations, check cultivars, and parental lines for agronomic and grain quality traits evaluated in four Iowa environments.

Population or group	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap [†]	Height cm
Check cultivars	378 a [‡]	1003 a	501 a	180 c	68 ab	84 ab	94 cd
Parental lines	319 b	910 b	501 a	190 b	67 cd	84 ab	98 ab
IABG1C0	361 a	1026 a	493 ab	184 c	67 bc	85 a	99 a
IABG1C1	381 a	1030 a	493 ab	193 ab	66 cd	83 ab	96 bc
IABG2C0	333 b	930 b	487 b	196 a	64 d	83 b	92 de
IABG2C1	271 c	772 c	477 c	196 a	65 cd	84 ab	92 e
IABGPI	342 ab	950 ab	467 c	191 ab	72 a	83 ab	97 abc

[†] Days after planting.

[‡] Means for the same trait followed by the same letter were not significantly different at P = 0.05 based on orthogonal contrasts.

Table 2. Agronomic and grain quality traits and rank among 95 entries of experimental oat lines with highest mean β -glucan content across environments and check cultivars from set one.

Line	β -Glucan content g kg ⁻¹	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
IA94031-6 [†]	69 (1) [‡]	292 (75)	826 (73)	483 (52)	207 (12)	59 (94)	84 (46)	89 (82)
IA95172-1 [§]	69 (2)	345 (48)	911 (56)	497 (27)	197 (30)	75 (20)	80 (88)	95 (52)
IA95109-2 [§]	69 (3)	309 (65)	795 (80)	479 (57)	195 (38)	65 (65)	86 (7)	83 (92)
IA95029-3 [§]	68 (4)	308 (67)	798 (79)	500 (22)	193 (40)	73 (24)	83 (64)	92 (72)
IA95148-3 [§]	68 (5)	287 (77)	770 (84)	487 (43)	190 (52)	64 (71)	84 (56)	86 (88)
IA95109-3 [§]	68 (6)	275 (84)	766 (85)	485 (44)	200 (25)	60 (91)	87 (2)	83 (91)
IA94190-10 [†]	68 (7)	371 (31)	980 (44)	504 (16)	188 (59)	67 (52)	80 (90)	92 (71)
IA93034-2 [§]	68 (8)	360 (36)	908 (58)	479 (58)	198 (28)	79 (4)	79 (93)	90 (77)
IA94190-1 [†]	67 (9)	403 (10)	1021 (26)	493 (34)	186 (68)	69 (42)	80 (89)	93 (63)
IA93029-6 [§]	66 (10)	351 (45)	995 (38)	491 (35)	179 (81)	59 (92)	83 (68)	96 (47)
Mean	68	330	877	490	193	67	83	90
Range	69-66	403-271	1021-766	504-479	207-186	79-59	87-79	96-83
IAN979-5-2 [¶]	64 (11)	356 (40)	991 (39)	464 (83)	190 (49)	78 (6)	88 (1)	90 (81)
Starter [#]	56 (54)	365 (33)	944 (50)	517 (5)	189 (54)	66 (55)	81 (82)	92 (69)
Hazel [#]	51 (72)	407 (7)	1045 (18)	496 (32)	187 (65)	81 (2)	83 (67)	92 (73)
Noble [#]	50 (76)	330 (58)	946 (49)	511 (9)	198 (29)	62 (79)	84 (43)	95 (49)
Don [#]	48 (78)	362 (34)	891 (65)	484 (49)	173 (91)	75 (19)	81 (79)	88 (85)
Ogle [#]	48 (79)	406 (8)	1140 (8)	471 (73)	184 (75)	66 (60)	84 (54)	96 (45)
Mean	53	371	993	490	187	71	83	92
Range	64-48	407-330	1140-891	517-464	198-173	81-62	88-81	96-88
Mean of all entries	58	342	942	489	190	67	84	95
LSD _{L vs L} ^{††}	4	64	155	30	9	4	2	5
LSD _{L vs C} ^{‡‡}	3	55	134	26	8	3	2	5
LSD _{C vs C} ^{§§}	1	45	109	21	7	3	2	4

[†], [§] Lines from IABG2C0 and IABG2C1, respectively.

[‡] Rank of genotypes within parenthesis.

[¶] Check line considered as a line for pair-wise comparisons.

[#] Check cultivar.

^{††}, ^{‡‡}, ^{§§} Least significant difference at the 0.05 probability level for pair-wise comparisons of line vs line, line vs check, and check vs check, respectively.

Table 3. Estimated components of variance and their standard deviations of five experimental oat populations, for agronomic and grain quality traits.

Trait	Source	IABG1C0	IABG1C1	IABG2C0	IABG2C1	IABGPI
<hr/>						
				$(g\ m^{-3})^2$		
Grain yield	Family	1878** (573) [†]	2433** (769)	2360** (647)	1549** (506)	581 (1770)
	Env x Family	171 (190)	269 (270)	84 (148)	225 (151)	266 (282)
	Line(Family)	805** (275)	472* (268)	1028** (298)	980** (284)	3364* (1715)
	Residual [‡]	2087** (245)	2118** (326)	1623** (192)	1446** (178)	1404** (301)
	$\sigma^2_f - \sigma^2_{l(f)}$ [§]	1073	NA [†]	NA	NA	NA
	$\sigma^2_f - 3\sigma^2_{l(f)}$	NA	1017	-724	-1391	NA
Biomass	Family	4452* (224)	8029** (3204)	6147** (1897)	9392** (2658)	7075 (6331)
	Env x Family	4495** (1434)	3038* (1456)	2127** (854)	851 (643)	562 (1725)
	Line(Family)	5211** (1636)	3055** (1448)	2596** (937)	4019** (1172)	7947** (4183)
	Residual	11111** (1317)	10052** (1505)	7232** (865)	6216** (765)	9149** (2047)
	$\sigma^2_f - \sigma^2_{l(f)}$	-759	NA	NA	NA	NA
	$\sigma^2_f - 3\sigma^2_{l(f)}$	NA	-1136	-1641	-265	NA
				$(kg\ m^{-3})^2$		
Test weight	Family	5 (48)	227** (78)	314** (98)	157* (74)	48 (71)
	Env x Family	10 (41)	0	136** (47)	0	49 (102)
	Line(Family)	197** (65)	30 (35)	103** (43)	175** (70)	52 (71)
	Residual	459 (55)	388 (41)	370 (45)	522 (49)	526** (115)
	$\sigma^2_f - \sigma^2_{l(f)}$	-192**	NA	NA	NA	NA
	$\sigma^2_f - 3\sigma^2_{l(f)}$	NA	137	5	-368	NA

Table 3. Estimated components of variance and their standard deviations of five experimental oat populations, for agronomic and grain quality traits (continued).

Trait	Source	IABG1C0	IABG1C1	IABG2C0	IABG2C1	IABGPI
(g kg ⁻¹) ²						
Protein content	Family	39** (17.0)	114** (33.0)	76** (20.0)	62** (16.0)	73* (33.0)
	Env x Family	1 (4.0)	11** (4.0)	12** (4.0)	14** (5.0)	1 (6.0)
	Line(Family)	57** (14.0)	17** (6.0)	27** (8.0)	11** (5.0)	11 (7.0)
	Residual	45 (5.0)	19 (3.0)	32 (4.0)	35 (5.0)	33** (8.0)
	$\sigma^2_r - \sigma^2_{l(f)}$	-18	NA	NA	NA	NA
	$\sigma^2_r - 3\sigma^2_{l(f)}$	NA	63	-5	29	NA
Oil content	Family	14** (5.0)	13** (5.0)	41** (9.0)	28** (7.0)	12 (9.0)
	Env x Family	1* (0.6)	1* (0.4)	1** (0.5)	1 (0.8)	4** (1.0)
	Line(Family)	11** (2.0)	10** (3.0)	7** (2.0)	9** (2.0)	10* (4.0)
	Residual	5 (0.6)	3 (0.4)	4 (0.5)	7 (1.0)	3** (1.0)
	$\sigma^2_r - \sigma^2_{l(f)}$	3	NA	NA	NA	NA
	$\sigma^2_r - 3\sigma^2_{l(f)}$	NA	-17	20	1	NA
dapr ²						
Heading date	Family	0.4 (0.5)	3.1** (1.1)	2.9** (0.9)	2.2** (0.8)	1.0 (1.0)
	Env x Family	0.1 (0.1)	0.5* (0.3)	0.5** (0.3)	0.3 (0.3)	0.0
	Line(Family)	2.5** (0.6)	1.4** (0.5)	1.2** (0.4)	1.5** (0.5)	1.6 (1.2)
	Residual	0.8** (0.1)	1.0** (0.3)	1.1** (0.2)	1.5** (0.3)	3.6** (0.9)
	$\sigma^2_r - \sigma^2_{l(f)}$	-2.0**	NA	NA	NA	NA
	$\sigma^2_r - 3\sigma^2_{l(f)}$	NA	-1.2	-0.9	-2.3	NA

Table 3. Estimated components of variance (and their standard deviations) of five experimental oat populations for agronomic and grain quality traits (continued).

Trait	Source	IABG1C0	IABG1C1	IABG2C0	IABG2C1	IABGPI
		cm ²				
Height	Family	10.7** (3.6)	9.2** (3.4)	14.1** (3.9)	25.1** (6.3)	38.0** (14.0)
	Env x Family	1.0 (0.8)	0.0	0.6 (1.0)	0.4 (1.5)	0.0
	Line(Family)	8.1** (2.1)	4.0** (1.6)	5.5** (1.8)	5.6** (2.3)	1.4 (1.9)
	Residual	4.2** (0.9)	4.7** (0.8)	5.9** (1.2)	9.7** (1.9)	7.0** (1.7)
	$\sigma^2_f - \sigma^2_{l(f)}$	2.5	NA	NA	NA	NA
	$\sigma^2_f - 3\sigma^2_{l(f)}$	NA	-2.8	-2.2	-8.4	NA

*,** Significant at the 0.05 and 0.01 probability level.

† Sampling standard deviations of components of variance estimates within parenthesis.

‡ Residual variance equals $\sigma^2_{\text{env} \times \text{line}(\text{family})} + (\sigma^2_{\text{error}})/2$ for grain yield, biomass, heading date, and height. Residual variance equals $\sigma^2_{\text{env} \times \text{line}(\text{family})} + \sigma^2_{\text{error}}$ for test weight and protein and oil content.

§ σ^2_f , $\sigma^2_{l(f)}$ Full-sib family variance and $S_{0:1}$ line within family variance, respectively.

¶ Not applicable (NA).

Table 4. Phenotypic and genetic variance component estimates and their standard deviations of four experimental oat populations.

Trait	Variance	IABG1C0	IABG1C1	Change	IABG2C0	IABG2C1	Change
		g^2m^{-4}		%	g^2m^{-4}		%
Grain yield	Phenotypic [†]	4591 (332) [‡]	4902 (438)	7	4858 (352)	4052 (306)	-17
	Genotypic [§]	2549 (469)	2703 (611)	6	3340 (554)	2455 (427)	-26
Biomass	Phenotypic	24350 (1790)	22758 (2035)	-6	17571 (1295)	19763 (1493)	12
	Genotypic	9305 (1997)	10241 (2492)	10	8549 (1613)	13108 (2192)	53
		kg^2m^{-6}			kg^2m^{-6}		
Test weight	Phenotypic	673 (50)	637 (59)	-5	884 (65)	854 (67)	-3
	Genotypic	203 (48)	253 (65)	25	406 (81)	333 (72)	-18
		g^2kg^{-2}			g^2kg^{-2}		
Protein content	Phenotypic	142 (11)	155 (14)	9	140 (11)	118 (9)	-16
	Genotypic	95 (16)	129 (24)	36	103 (17)	77 (14)	-25
Oil content	Phenotypic	31 (2)	26 (2)	-16	50 (4)	44 (3)	-12
	Genotypic	24 (4)	22 (4)	-8	46 (7)	35 (6)	-24
		dap^2			dap^2		
Heading date	Phenotypic	3.7 (0.4)	5.7 (0.7)	54**	5.5 (0.6)	5.3 (0.5)	-4
	Genotypic	2.9 (0.5)	4.3 (0.9)	48	4.0 (0.7)	3.9 (0.7)	-2

Table 4. Phenotypic and genetic variance component estimates and their standard deviations of four experimental oat populations (continued).

Trait	Variance	IABG1C0	IABG1C1	Change	IABG2C0	IABG2C1	Change
		cm ²		%	cm ²		%
Height	Phenotypic	23 (2)	17 (2)	-26*	26 (3)	41 (4)	58*
	Genotypic	18 (3)	12 (3)	-33	19 (3)	30 (5)	58†

† Phenotypic variance estimated as: $\sigma^2_p = \sigma^2_{\text{family}} + \sigma^2_{\text{line(family)}} + \sigma^2_{\text{env} \times \text{family}} + \sigma^2_{\text{residual}}$.

Residual variance equals $\sigma^2_{\text{env} \times \text{line(family)}} + (\sigma^2_{\text{error}})/2$ for grain yield, biomass, heading date and height. Residual variance equals $\sigma^2_{\text{env} \times \text{line(family)}} + \sigma^2_{\text{error}}$ for test weight and protein and oil content.

‡ Sampling standard deviations of variance estimates within parenthesis.

§ Genotypic variance estimated as: $\sigma^2_G = \sigma^2_{\text{family}} + \sigma^2_{\text{line(family)}}$.

¶ Significant at the 0.07 probability level.

Table 5. Heritabilities and their standard deviations of agronomic and grain quality traits for five experimental oat populations evaluated in four Iowa environments.

Population	Grain yield	Biomass	Test weight	Protein content	Oil content	Heading date	Height
H^2 on a plot or a sample-basis [†]							
IABG1C0	0.35 (0.03) [‡]	0.27 (0.03)	0.30 (0.05)	0.67 (0.08)	0.79 (0.10)	0.55 (0.05)	0.39 (0.04)
IABG1C1	0.33 (0.04)	0.30 (0.04)	0.40 (0.06)	0.82 (0.13)	0.86 (0.14)	0.61 (0.08)	0.56 (0.07)
IABG2C0	0.45 (0.04)	0.35 (0.03)	0.45 (0.05)	0.70 (0.08)	0.90 (0.12)	0.55 (0.05)	0.59 (0.06)
IABG2C1	0.43 (0.04)	0.21 (0.03)	0.39 (0.05)	0.62 (0.07)	0.81 (0.11)	0.53 (0.05)	0.63 (0.06)
IABGPI	0.50 (0.08)	0.39 (0.06)	0.61 (0.11)	0.67 (0.14)	0.74 (0.16)	0.46 (0.08)	0.76 (0.16)
H^2 on a line mean-basis [§]							
IABG1C0	0.82 (0.03)	0.71 (0.04)	0.46 (0.06)	0.89 (0.03)	0.94 (0.03)	0.87 (0.06)	0.93 (0.04)
IABG1C1	0.82 (0.04)	0.76 (0.05)	0.57 (0.06)	0.95 (0.04)	0.96 (0.04)	0.85 (0.08)	0.91 (0.05)
IABG2C0	0.88 (0.03)	0.79 (0.03)	0.62 (0.05)	0.90 (0.03)	0.97 (0.04)	0.83 (0.06)	0.92 (0.04)
IABG2C1	0.85 (0.03)	0.88 (0.03)	0.56 (0.05)	0.87 (0.04)	0.95 (0.04)	0.80 (0.06)	0.92 (0.04)
IABGPI	0.90 (0.06)	0.85 (0.06)	0.75 (0.09)	0.89 (0.06)	0.92 (0.06)	0.84 (0.20)	0.95 (0.06)

Table 5. Heritabilities and their standard deviations of agronomic and grain quality traits for five experimental oat populations evaluated in four Iowa environments (continued).

Population	Grain yield	Biomass	Test weight	Protein content	Oil content	Heading date	Height
H² on a family mean-basis[¶]							
IABG1C0	0.73 (0.08)	0.46 (0.15)	0.03 (0.29)	0.53 (0.14)	0.70 (0.09)	0.23 (0.22)	0.65 (0.10)
IABG1C1	0.81 (0.07)	0.69 (0.11)	0.78 (0.08)	0.89 (0.04)	0.71 (0.10)	0.71 (0.10)	0.74 (0.09)
IABG2C0	0.76 (0.07)	0.69 (0.08)	0.70 (0.08)	0.78 (0.06)	0.90 (0.03)	0.71 (0.08)	0.76 (0.07)
IABG2C1	0.68 (0.09)	0.76 (0.07)	0.51 (0.15)	0.82 (0.05)	0.83 (0.05)	0.64 (0.11)	0.82 (0.05)
IABGPI	0.23 (0.60)	0.57 (0.28)	0.90 (0.05)	0.88 (0.07)	0.66 (0.21)	0.37 (0.32)	0.94 (0.03)

† Heritability on a plot-basis estimated as: $(\sigma^2_{\text{family}} + \sigma^2_{\text{line(family)}})/(\sigma^2_{\text{family}} + \sigma^2_{\text{line(family)}} + \sigma^2_{\text{env}} \times \text{family} + \sigma^2_{\text{experimental error}})$ for grain yield, biomass, heading date, and height. Heritability on a sample-basis estimated as: $(\sigma^2_{\text{family}} + \sigma^2_{\text{line(family)}})/(\sigma^2_{\text{family}} + \sigma^2_{\text{line(family)}} + \sigma^2_{\text{env}} \times \text{family} + \sigma^2_{\text{residual}})$ for test weight and protein and oil content. Residual variance equals $\sigma^2_{\text{env}} \times \text{line(family)} + \sigma^2_{\text{error}}$.

‡ Sampling standard deviations of heritability estimates within parenthesis.

§ Heritability on line mean-basis estimated as: $(\sigma^2_{\text{family}} + \sigma^2_{\text{line(family)}})/[\sigma^2_{\text{family}} + \sigma^2_{\text{line(family)}} + (\sigma^2_{\text{env}} \times \text{family} + \sigma^2_{\text{residual}})/4]$ for grain yield, biomass, test weight, protein and oil; and estimated as: $(\sigma^2_{\text{family}} + \sigma^2_{\text{line(family)}})/[\sigma^2_{\text{family}} + \sigma^2_{\text{line(family)}} + (\sigma^2_{\text{env}} \times \text{family} + \sigma^2_{\text{residual}})/2]$ for heading date and height.

¶ Heritability on family mean-basis estimated as: $\sigma^2_{\text{family}}/[\sigma^2_{\text{family}} + \sigma^2_{\text{line(family)}}/2 + \sigma^2_{\text{env}} \times \text{family}/4 + \sigma^2_{\text{residual}}/8]$ for grain yield, biomass, test weight, protein and oil, and estimated as: $\sigma^2_{\text{family}}/[\sigma^2_{\text{family}} + \sigma^2_{\text{line(family)}}/2 + \sigma^2_{\text{env}} \times \text{family}/2 + \sigma^2_{\text{residual}}/4]$ for heading date and height. Residual variance equals $\sigma^2_{\text{env}} \times \text{line(family)} + (\sigma^2_{\text{error}})/2$ for grain yield, biomass, heading date, and height. Residual variance equals $\sigma^2_{\text{env}} \times \text{line(family)} + \sigma^2_{\text{error}}$ for test weight and protein and oil content.

Table 6. Estimates and standard errors of genotypic and phenotypic correlations between β -glucan content and agronomic and grain quality traits for five experimental oat populations evaluated in four Iowa environments.

Population or group	Grain yield	Biomass	Test weight	Protein content	Oil content	Heading date	Height
Genotypic correlation [†]							
IABG1C0	0.31 (0.12) [‡]	0.15 (0.14)	-0.21 (0.14)	0.32 (0.11)	-0.12 (0.12)	-0.10 (0.13)	-0.11 (0.13)
IABG1C1	-0.25 (0.15)	-0.16 (0.16)	-0.01 (0.17)	0.15 (0.14)	-0.13 (0.14)	-0.39 (0.15)	-0.21 (0.15)
IABG2C0	-0.15 (0.12)	-0.28 (0.12)	-0.13 (0.13)	0.08 (0.12)	-0.24 (0.11)	0.18 (0.14)	0.29 (0.13)
IABG2C1	-0.49 (0.11)	-0.49 (0.11)	-0.14 (0.15)	0.30 (0.12)	-0.28 (0.11)	0.27 (0.17)	0.19 (0.16)
IABGPI	0.04 (0.21)	-0.06 (0.23)	0.24 (0.45)	0.06 (0.21)	-0.18 (0.20)	0.38 (0.31)	0.01 (0.22)
Phenotypic correlation [§]							
IABG1C0	0.16 (0.07)	0.05 (0.07)	-0.11 (0.07)	0.26 (0.07)	-0.10 (0.08)	-0.03 (0.09)	-0.11 (0.09)
IABG1C1	-0.05 (0.09)	0.04 (0.09)	-0.02 (0.09)	0.14 (0.10)	-0.14 (0.10)	-0.19 (0.11)	-0.17 (0.11)
IABG2C0	-0.09 (0.08)	-0.15 (0.07)	-0.06 (0.07)	0.05 (0.08)	-0.17 (0.08)	0.09 (0.10)	0.15 (0.10)
IABG2C1	-0.21 (0.07)	-0.21 (0.07)	-0.01 (0.08)	0.20 (0.07)	-0.20 (0.08)	0.13 (0.10)	0.06 (0.10)
IABGPI	0.10 (0.14)	0.08 (0.13)	0.05 (0.11)	0.07 (0.14)	-0.15 (0.14)	0.29 (0.15)	0.09 (0.17)

Table 6. Estimates and standard errors of genotypic and phenotypic correlations between β -glucan content and agronomic and grain quality traits for five experimental oat populations evaluated in four Iowa environments. (continued).

Population or group	Grain yield	Biomass	Test weight	Protein content	Oil content	Heading date	Height
Phenotypic correlation [¶]							
IABG1C0	0.24 (0.10)	0.10 (0.10)	-0.16 (0.10)	0.30 (0.09)	-0.11 (0.10)	-0.06 (0.10)	-0.11 (0.10)
IABG1C1	-0.17 (0.12)	-0.08 (0.13)	-0.01 (0.13)	0.15 (0.12)	-0.13 (0.12)	-0.26 (0.12)	-0.18 (0.12)
IABG2C0	-0.13 (0.10)	-0.23 (0.10)	-0.10 (0.10)	0.07 (0.10)	-0.21 (0.10)	0.13 (0.10)	0.20 (0.10)
IABG2C1	-0.37 (0.09)	-0.37 (0.09)	-0.08 (0.10)	0.25 (0.10)	-0.25 (0.10)	0.18 (0.11)	0.10 (0.11)
IABGPI	0.06 (0.18)	0.002 (0.18)	0.10 (0.18)	0.06 (0.18)	-0.17 (0.18)	0.31 (0.17)	0.06 (0.18)

† Genotypic correlation estimated as: $\sigma_{\text{line w,z}} / (\sigma_{\text{line w}}^2 \sigma_{\text{line z}}^2)^{1/2}$.

‡ Sampling standard deviations of heritability estimates within parenthesis.

§ Phenotypic correlation estimated on a sample-basis as: $(\sigma_{\text{line w,z}} + \sigma_{\text{residual w,z}}) / [(\sigma_{\text{line w}}^2 + \sigma_{\text{residual w}}^2)(\sigma_{\text{line z}}^2 + \sigma_{\text{residual z}}^2)]^{1/2}$.

¶ Phenotypic correlation estimated on a line mean-basis as: $[\sigma_{\text{line w,z}} + (\sigma_{\text{residual w,z}})/4] / \{[\sigma_{\text{line w}}^2 + (\sigma_{\text{residual w}}^2)/4][\sigma_{\text{line z}}^2 + (\sigma_{\text{residual z}}^2)/4]\}^{1/2}$ for yield, biomass, test weight, and protein and oil content, and estimated as: $[\sigma_{\text{line w,z}} + (\sigma_{\text{residual w,z}})/2] / \{[\sigma_{\text{line w}}^2 + (\sigma_{\text{residual w}}^2)/2][\sigma_{\text{line z}}^2 + (\sigma_{\text{residual z}}^2)/2]\}^{1/2}$ for heading date and height.

Residual covariance equals $\sigma_{\text{env} \times \text{line(family)} \text{ w,z}} + \sigma_{\text{error w,z}}$. Residual variance equals $\sigma_{\text{env} \times \text{line(family)}}^2 + (\sigma_{\text{error}}^2)/2$ for grain yield, biomass, heading date, and height. Residual variance equals $\sigma_{\text{env} \times \text{line(family)}}^2 + \sigma_{\text{error}}^2$ for test weight and protein and oil content.

Residual variance equals $\sigma_{\text{env} \times \text{line(family)}}^2 + (\sigma_{\text{error}}^2)/2$ for grain yield, biomass, heading date, and height. Residual variance equals $\sigma_{\text{env} \times \text{line(family)}}^2 + \sigma_{\text{error}}^2$ for test weight and protein and oil content.

CHAPTER 5. CONCLUSIONS

One generation of phenotypic selection of field-grown S_0 plants for greater β -glucan content increased the mean of this trait in the IABG1 and IABG2 oat populations by 11 and 4 %, respectively. The intermediate heritability, the predominantly additive inheritance and the abundant genetic variability of the trait along with the availability of instruments to rapidly measure groat β -glucan concentration allowed rapid improvements to be made with single plant phenotypic selection. Furthermore, β -glucan content of improved genotypes was stable across the environments in which this study was conducted, indicating that selections made in only one environment might be expected to result in improvements realized in other similar environments.

However, selection for high β -glucan content in IABG2 reduced the mean grain yield, biomass, and test weight by 19, 17, and 2%, respectively. The genetic variance of grain quality and agronomic traits was generally not affected. The magnitude of the negative genotypic correlations between β -glucan content and grain yield, biomass, and test weight became larger (more unfavorable) following selection for greater β -glucan content, and this likely contributed to the unfavorable correlated changes in the IABG2 population mean. Strategies for selecting agronomic traits simultaneously with β -glucan content should be implemented. Selection for greater β -glucan yield is a possibility to improve β -glucan content without decreasing grain yield. The germplasm lines with elevated β -glucan content developed from this program should prove useful as breeding parents for cultivar development programs.

APPENDIX A. POPULATION DEVELOPMENT

Development of IABG1 oat population

The original population was developed by the intermating of commercial oat varieties and breeding lines chosen for their high β -glucan content or good agronomic characteristics (Table 1, Table 2). In the spring of 1990, 17 crosses were made among 14 cultivars and lines in the greenhouse. Plants were crossed using the approach method (McDaniel et al. 1967). The progenies of these crosses were denominated N975-N996 (Table 3). In the fall of 1990, double crosses were performed among the N975-N996 crosses in the greenhouse, their progenies were denominated P301-P308. In the fall of 1991, forty-two crosses were made in the greenhouse between the P302-P308 crosses and nine S_0 's developed at the University of Minnesota from crosses among high β -glucan experimental lines and cultivars (MN1-88106 - MN9-88177) (Table 2). These crosses were denominated IA91431 - IA91472. In addition forty-three crosses were made among the same P302-P308 crosses and eleven S_0 parents (C05937 - C05960) developed by Agricultural Canada in Ottawa from crosses made among high β -glucan experimental lines and the cultivar Premier (Table 2). These crosses were denominated IA91473 - IA91515. Twelve crosses also were made among the P302-P308 (excluding P305) S_0 's and denominated IA1524 - IA91535 (Table 3). The S_0 seed obtained from these 97 crosses (IA91431-IA91535) constituted the base population for selection, IABG1C0 (Figure 1).

Table 1. Lines and cultivars used to develop the IABG1C0 population

Line	Source	Line	Source
C05937 [†]	Ag. Canada, Ottawa	Hazel [‡]	Univ. of Illinois
C05938 [†]	Ag. Canada, Ottawa	IL82-2154	Univ. of Illinois
C05939 [†]	Ag. Canada, Ottawa	IL85-61831	Univ. of Illinois
C05942 [†]	Ag. Canada, Ottawa	MN1-88106	Univ. of Minnesota
C05943 [†]	Ag. Canada, Ottawa	MN2-88107 [§]	Univ. of Minnesota
C05949 [†]	Ag. Canada, Ottawa	MN3-88125 [§]	Univ. of Minnesota
C05952 [†]	Ag. Canada, Ottawa	MN4-88127 [§]	Univ. of Minnesota
C05953 [†]	Ag. Canada, Ottawa	MN5-88153 [§]	Univ. of Minnesota
C05954 [†]	Ag. Canada, Ottawa	MN6-88163 [§]	Univ. of Minnesota
C05957 [†]	Ag. Canada, Ottawa	MN7-88174 [§]	Univ. of Minnesota
C05960 [†]	Ag. Canada, Ottawa	MN8-88176 [§]	Univ. of Minnesota
D831-1-571	Iowa State Univ.	MN9-88177 [§]	Univ. of Minnesota
D921-255	Iowa State Univ.	MN86226	Univ. of Minnesota
H52-5	Iowa State Univ.	MO07929	Univ. of Missouri
H87-7-4	Iowa State Univ.	P786D1-5-5-2-10-1	Purdue Univ.
H730-12	Iowa State Univ.	Premier [‡]	Univ. of Minnesota
H688-11	Iowa State Univ.	Starter [†]	Univ. of Minnesota

[†] S₀'s from double crosses.

[‡] Commercial cultivars.

[§] S₀'s from 7-way crosses.

In 1992, in Aberdeen, Idaho, 1665 S₀ plants (from two to thirty-eight per cross) from IABG1C0 were grown as spaced plants in the field. The S₁ seed of each S₀ plant was harvested individually and analyzed for β -glucan content via automated flow injection analysis (FIA). The β -glucan value of each plant was the mean of three subsamples and three individual determinations per each subsample. Forty C₀ S_{0:1} lines with highest β -glucan contents representing twenty-one full sib families were selected to be parents of the IABG1C1 population. 116 crosses among IABG1C0 parents were made to develop the

Table 2. Parents of the S_0 's developed by the University of Minnesota and Agricultural Canada that were used to develop the IABG1C0 population

Parents of Minnesota lines	Parents of Ottawa lines
Marion	Premier
Premier	NO4-8
Starter	NO5-1
Pur. 869D1-5-3-2-10-1	NO11-1
MN 86226	NO10-1
MN 88156	NO20-1
MN 88231	O5406...380
	OA926-2

IABG1C1 population (Figure 1). In 1993, in Aberdeen, ID, 582 S_0 plants from these crosses were grown as space plants in field and harvest individually to form $S_{0,1}$ lines.

Development of IABG2 population

In the summer of 1991, four crosses were made among plant introductions (PI's) and elite experimental lines or the cultivar Premier. These crosses were denominated IA91112 - IA91114 and IA91539. In spring of 1992, ten additional crosses were made between ten PI's and the IA91112-IA91114, IA91539 crosses or cultivars Marion or Premier. They were denominated IA92001 - IA920010 (Table 4).

Table 3. Crosses made to develop the IABG1C0 base population.

Year	Parent 1	Parent 2	Cross denomination
1990	Starter	Hazel	N975
	MN86226	H52-5	N976
	Starter	D921-255	N977
	IL85-6183-1	MO07929	N979
	MO07929	D921-255	N982
	Premier	D831-1-571	N983
	D831-1-541	P7869D1-5-5-2-10-1	N984
	Starter	MN86226	N985
	MN86226	H688-11	N986
	H730-12	P7869D1-5-5-2-10-1	N987
	Starter	IL85-6183-1	N988
	P7869D1-5-5-2-10-1	IL82-2154	N989
	Starter	H730-12	N990
	Premier	P7869D1-5-5-2-10-1	N991
	Premier	I182-2154	N992
	MN86226	MO07929	N993
	Premier	H87-7-4	N996
1990	N986	N988	P301
	N996	N988	P302
	N993	N990	P303
	N996	N992	P304
	N983	N982	P305
	N985	N982	P306
	N979	N977	P307
	N976	N975	P308
1991	PI302 – P308	MN1 – MN9	IA91431 – IA91472 [†]
	C05937 – C05960	P302 – P308	IA91473 – IA91515 [‡]
	P302 – P307 [§]	P302 – P308 [§]	IA91524 – IA91535 [¶]

[†] Forty-two crosses.

[‡] Forty-three crosses.

[§] P305 is not included.

[¶] Twelve crosses.

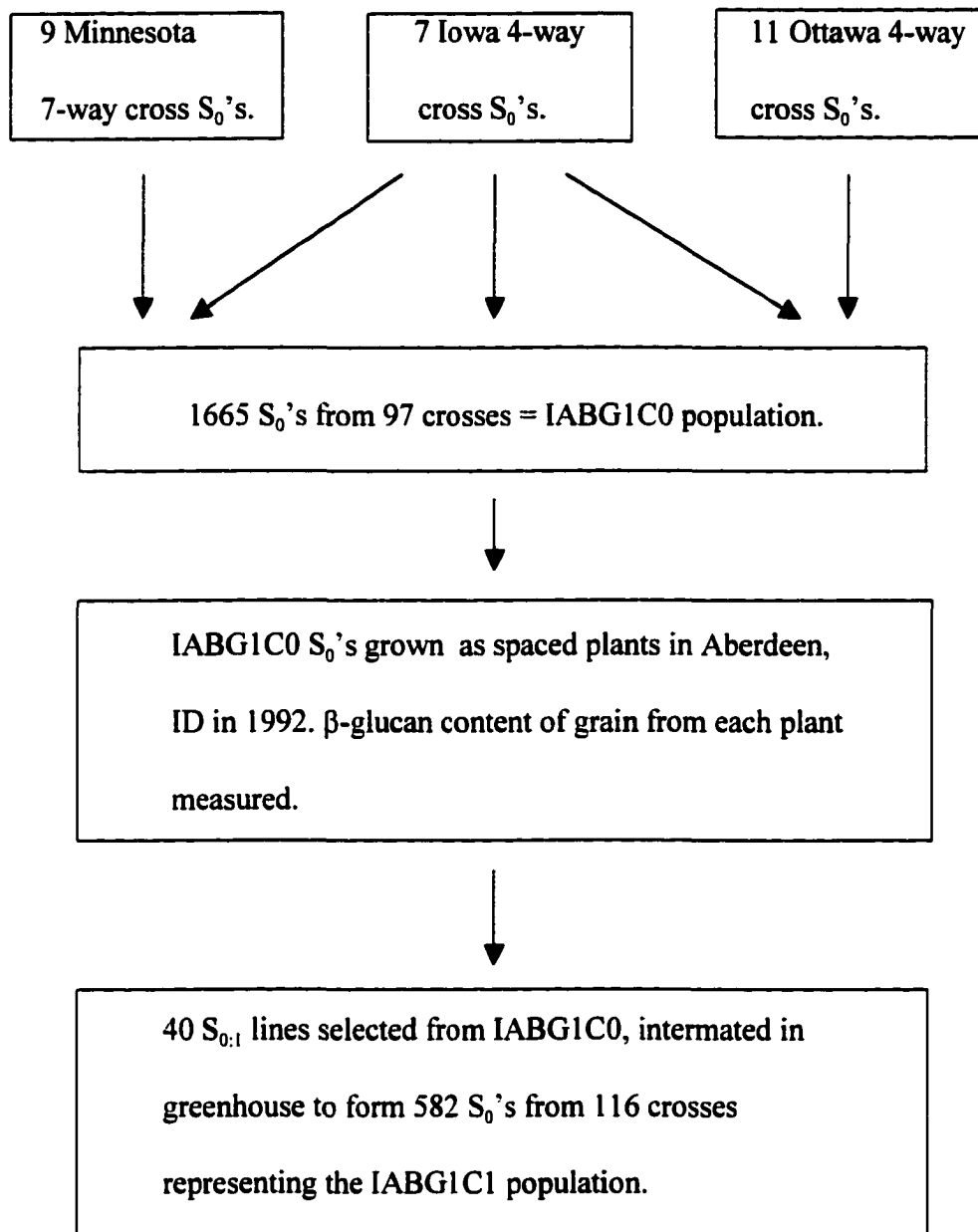


Figure 1. Development of the IABG1C0 and IABG1C1 populations.

Table 4. Crosses involving plant introductions that contributed to IABGPI and IABG2C0

Populations.	
Cross	Pedigree
IA92001	PI361884 (from Romania)//PI412689 (from Turkey)/IL85-6183-1
IA92002	PI412928 (from South Africa)//PI412689 (from Turkey)/IL85-6183-1
IA92003	PI504601 (from ok)//PI411649 (<i>A. sterilis</i> from Eritrea) /MO07929
IA92004	PI504611 (from Penn. State Univ.)// PI411649 (<i>A. sterilis</i> from Eritrea) /MO07929
IA92005	PI361886 (from Romania)//PI309123 (<i>A. sterilis</i> from Israel)/H87-24
IA92006	PI504593 (from Penn. State Univ.)// PI309123 (<i>A. sterilis</i> from Israel) /H87-24
IA92007	PI502955 (from Iowa State Univ.)//PI295903 (<i>A. sterilis</i> from Israel) /IA91539
IA92008	Marion// PI295903 (<i>A. sterilis</i> from Israel)/IA91539
IA92009	PI309598 (<i>A. sterilis</i> from Israel)//Premier
IA92010	PI412418 (<i>A. sterilis</i> from Israel)//Premier

S₀ plants representing the ten 25%, 50% and 75% PI-parentage crosses (Table 4) were mated to the same 40 S₀:1 lines selected from IABG1C0 that were used as parents of IABG1C1. 369 S₀'s representing seventy-nine full-sib families were generated to form the IABGPI population (Figure 2).

The 369 S₀ plants from IABGPI were grown as spaced plants in Aberdeen, 1993 in the same experiment as the IABG1C1 population. A total of 951 C₁ S₀ plants (from one to ten per full sib family) representing the IABG1C1 and IABGPI populations combined were evaluated. The S₁ seed of each plant was harvested individually and analyzed for β-glucan

content via automated flow injection analysis (FIA). The β -glucan value of each plant was the mean of three subsamples and three individual determinations per each subsample.

Thirty-eight $S_{0:1}$ lines representing thirty-one full-sib families from the IABG1C1 population and seven full-sib families from the IABGPI populations were selected to be used as parents of a second population (IABG2). In addition, three $F_{2:6}$ lines with high β -glucan content from the original N975-N996 crosses were selected for the same purpose from a separate experiment. Nine IABG1C₀ $S_{0:1}$ lines that were not used as parents of the IABG1C1 population, but had relatively high β -glucan content, and the cultivar Marion were also selected to be parents for the IABG2C0 population, giving a total of fifty parents. The fifty parent lines were intermated in the greenhouse in spring of 1994 using the circular method. Each parent was used approximately ten times, resulting in a total of 248 crosses, constituting the IABG2C0 population (Figure 2).

In 1994, in Aberdeen, Idaho, 916 IABG2C0 S_0 plants (from one to ten per full sib family) were grown as spaced plants. The S_1 seed of each S_0 plant was harvested individually and analyzed for β -glucan content with the automated flow injection analysis (FIA). The β -glucan value of each plant was the mean of three subsamples and three individual determinations per each subsample. The mean β -glucan content of each family was computed, and a single line with highest β -glucan content within each of the fifty families with highest mean β -glucan contents were selected. Fifty IABG2C0 $S_{0:1}$ lines representing fifty full-sib families were selected to be parents of the IABG2C1 population. The selected lines were intermated in the greenhouse in spring of 1995 using the circular method. Each

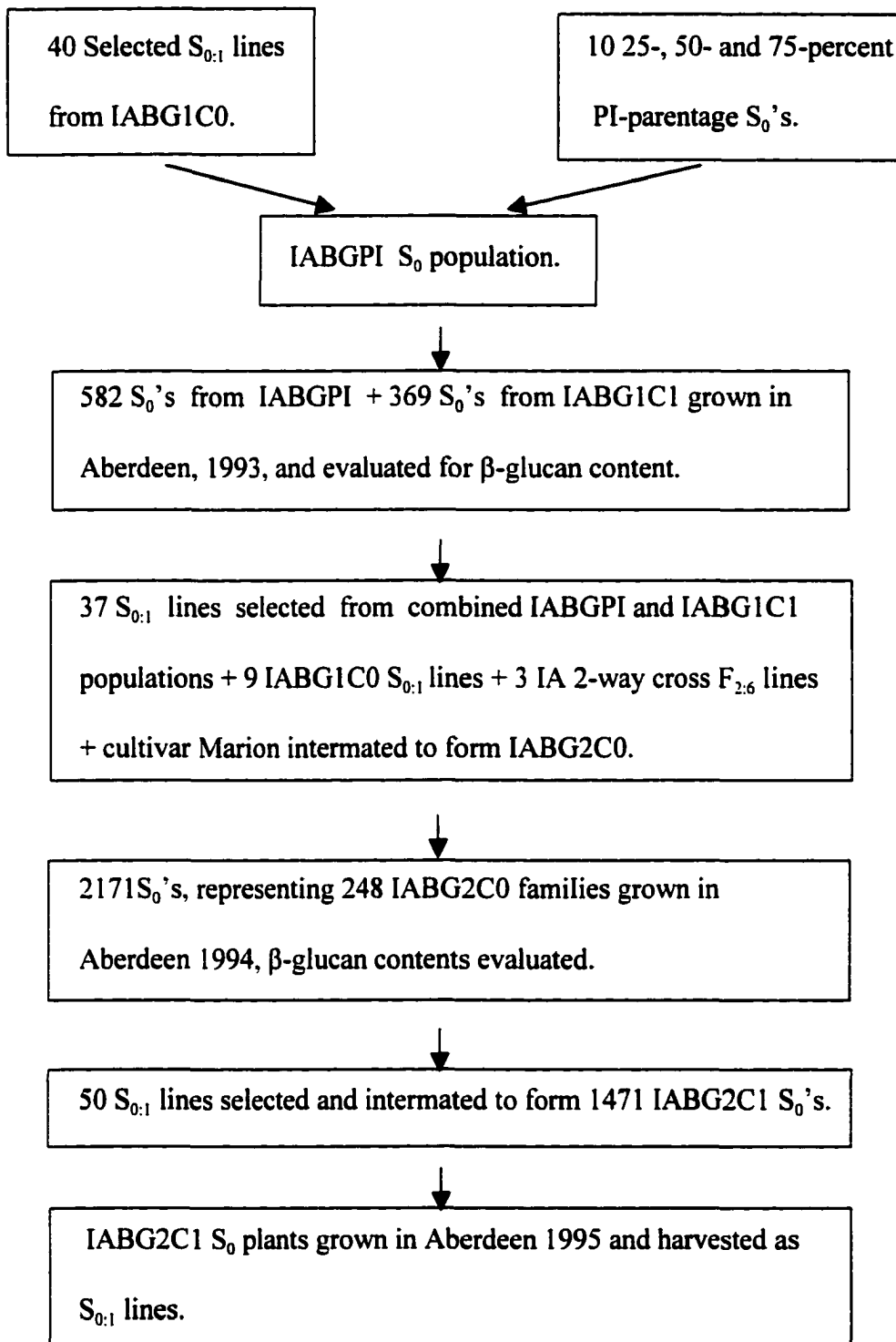


Figure 2. Development of the IABG2C0 and IABG2C1 populations.

parent was used ten times. A total of 250 crosses denominated IA95021-IA95270 were made and a total of 1471 S_0 seeds constituted the IABG2C1 population. 1471 S_0 plants were grown as spaced plants in Aberdeen, ID in summer of 1995; each plant was harvested individually to form $S_0:1$ lines (Figure 2).

APPENDIX B. GRAIN QUALITY ANALYSES

All oat samples were dehulled using a Codema Laboratory Dehuller (model LH 5095) to obtain approximately 8 g of groats. To inactivate endogenous enzymes, the samples were dried at 70 °C for 18 hr. The β -glucan, protein and oil contents of each groat sample were determined with a near-infrared reflectance spectrophotometer (NIRS) (Pacific Scientific Model 6250). The β -glucan, protein and oil values for each sample were the mean of three NIRS measurements. β -glucan content of 92 samples from the 1996 evaluation and 95 samples from the 1997 evaluation, representing 1% and 10% of the total number of samples from each year's evaluation, respectively, were measured with the automated flow injection analysis (FIA) to calibrate the prediction equation for β -glucan content for each year's evaluation. Protein contents of 52 samples (3% of the total number of samples) were measured using the Kjeldahl procedure to calibrate the prediction equation for protein content. Oil content of 74 samples from the 1996 evaluation and 99 samples from the 1997 evaluation, representing 8% and 11% of the total number of samples from each year, respectively, were determined by Nuclear Magnetic Resonance (Conway and Earle 1963) performed at the University of Illinois to calibrate the prediction equation for protein for each year evaluation.

Each FIA β -glucan determination was the mean of nine values: three subsamples were taken from each sample and three determinations were obtained for each subsample. The fluorometric FIA method was begun by extracting the water soluble β -glucan. The procedure used was previously described by Lim et al. (1992). Eight-g groat samples were

ground and the dry-basis sample weights were obtained for each sample. Next, approximately 100 mg of flour of each sample were placed in a screw cap test tube with a solution of 4.9 ml of water and 0.1 ml of α -amylase, sealed and heated with stirring in water at 100 °C for one h and then cooled in water for ten minutes. After adding 0.5 ml of 0.075 M H_2SO_4 , the tubes were heated with stirring for exactly ten minutes in water at 100 °C and cooled in water for ten minutes. The samples were transferred to polypropylene tubes and centrifuged for 11 minutes. Three subsamples of 0.5 ml aliquots of the supernatant from each sample were transferred to cultured tubes and diluted to 3 ml with distilled water.

The equipment for measuring β -glucan content using FIA consisted of a random sampler, pump, injection module, fluorescence spectrophotometer (Hitachi F-1050) and a computer. Each sample was mixed with a carrier buffer (0.1M tris solution) and conducted by the pump into the injection module where it was mixed with the fluorescence color reagent (0.005% cellufluor solution) and carried from there to the fluorescence spectrophotometer to monitor the increase in fluorescence intensity, which was recorded by the computer. The maximum increase in intensity (peak area) was recorded. Standards with known amounts of β -glucan were used to calculate the β -glucan content measurements. The peak area of each sample was converted to milligrams of β -glucan per liter using a regression equation obtained with calibration standards (Lim et al. 1992, Jørgensen 1988).

The Kjeldahl method to determine protein content (Bremmer and Breitenbeck 1983) involves digesting samples and determining the ammonium-N from the digests. For the first part of the procedure, samples of oat flour were poured into digestion tubes. Digestions were catalyzed by adding 3.5 ml of concentrated sulfuric acid to each tube. The tubes were placed

in racks, containing 36 tubes with oat samples, 2 blank tubes (no sample material), one forage standard, and one lysine standard. The rack was placed in the digestion block. All the samples were then digested for 3 hr and then cooled with cold water. 15 ml of ammonia-free water were added to each tube and the tubes were swirled to mix their content. The determination of ammonium N in the diluted digests was performed as follows: 5 ml of boric acid-indicator solution were added to an Erlenmeyer flask which later was placed under the condenser of a distillation apparatus. 15 ml of 10 N NaOH were added to the digestion tubes. Each tube was connected to the distillation apparatus. Steam distillation was conducted until 15 ml of distillate were collected. The ammonium-N was determined by titration with 0.01 N H_2SO_4 at 10 ml intervals. The color change of the distillate at the endpoint was from green to pink. Individual moisture determinations were not made because not enough sample material was available. Samples were equilibrated to about 10% moisture. The percentage crude protein was obtained by multiplying the percentage nitrogen by 6.25.

APPENDIX C. GENETIC EXPECTANCIES

The covariance of individuals X and Y was given by Weir and Cockerham (1976) as:

$$C_{XY} = 2\theta_{XY}\sigma_A^2 + 2\delta_{\bar{X}+\bar{Y}}\sigma_D^2 + 2(\gamma_{\bar{X}Y} + \gamma_{X\bar{Y}})\sum_i p_i \alpha_i \delta_{ii} + \delta_{\bar{X}\bar{Y}} \sum_i p_i \delta_{ii}^2 + (\delta_{\bar{X}\bar{Y}} - F_X F_Y) \left(\sum_i p_i \delta_{ii} \right)^2,$$

Cockerham (1983) introduced the following nomenclature for the non-additive genetic components of variance:

$$D_1 = \sum_i p_i \alpha_i d_{ii}$$

$$D_2 = \sum_i p_i d_{ii}^2 - \left(\sum_i p_i d_{ii} \right)^2$$

$$H = \left(\sum_i p_i d_{ii} \right)^2$$

D_1 represents the covariance between average allelic effects and their corresponding homozygous dominance deviations. D_2 represents the variance of homozygous dominance deviations. H represents the squared inbreeding depression effects at each locus.

Rearranging the previous equation to use these terms leads to:

$$C_{XY} = 2\theta_{XY}\sigma_A^2 + 2\delta_{\bar{X}+\bar{Y}}\sigma_D^2 + 2(\gamma_{\bar{X}Y} + \gamma_{X\bar{Y}})D_1 + \delta_{\bar{X}\bar{Y}}D_2 + (\delta_{\bar{X}\bar{Y}} - F_X F_Y)H.$$

The coefficients of the genetic components of variation are the identity by descent measures developed by Cockerham (1971). If individual X has alleles a and b at a locus and individual Y has alleles a' and b' at a locus, and the symbol \equiv is taken to mean identity by descent, the identity by descent measures for X and Y are:

$$\theta_{XY} = P(a \equiv a') = P(a \equiv b') = P(b \equiv a') = P(b \equiv b')$$

$$\gamma_{\ddot{X}Y} = P(a \equiv b \equiv a')$$

$$\gamma_{X\ddot{Y}} = P(a \equiv b \equiv b')$$

$$\delta_{\ddot{X}\ddot{Y}} = P(a \equiv b \text{ and } a' \equiv b' \text{ and } a \neq a')$$

$$\delta_{\ddot{X}+\ddot{Y}} = P(a \equiv a' \text{ and } a' \equiv b' \text{ and } a \neq b) = P(a \equiv b' \text{ and } b \equiv a' \text{ and } a \neq b)$$

$$\delta_{\ddot{X}\ddot{Y}} = P(a \equiv b \equiv a' \equiv b')$$

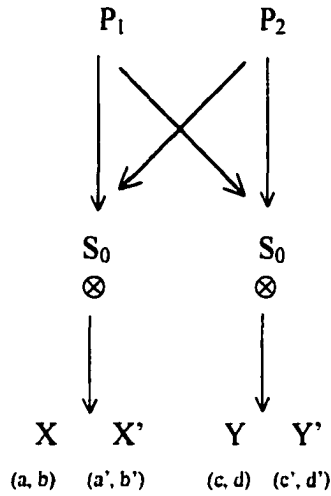
$$\Delta_{\ddot{X}\ddot{Y}} = P(a \equiv b \text{ and } a' \equiv b') = \delta_{\ddot{X}\ddot{Y}} + \delta_{\ddot{X}+\ddot{Y}}$$

The covariance of relatives can be extended to include non-allelic interactions as follows:

$$\begin{aligned} C_{XY} = & 2\theta_{XY}\sigma_A^2 + 2\delta_{\ddot{X}+\ddot{Y}}\sigma_D^2 + 2(\gamma_{\ddot{X}Y} + \gamma_{X\ddot{Y}})D_1 + \delta_{\ddot{X}\ddot{Y}}D_2 + (\Delta_{\ddot{X}\ddot{Y}} - F_X F_Y)H + (2\theta_{XY}\sigma_A^2)^2\sigma_{AA}^2 \\ & + (2\delta_{\ddot{X}+\ddot{Y}})^2\sigma_{DD}^2 + (2\theta_{XY})(2\delta_{\ddot{X}+\ddot{Y}})\sigma_{AD}^2 + \dots \end{aligned}$$

Turning to the problem of this study, that is, the covariance of relatives in this experiment, there are two types of relatives for which we need to derive the covariance of relatives: S₁ progeny descended from the same S₀ plant, and S₁ progeny from the same full-sib family but descended from different S₀ plants.

The mating design used to obtain the $S_{0:1}$ lines evaluated can be represented as:



The probabilities of identity by descent for the alleles of the individuals X and X' are:

$$\theta_{XX'} = P(a \equiv a') = P(a \equiv b') = P(b \equiv a') = P(b \equiv b') = 1/2,$$

$$\gamma_{XX'} = P(a \equiv b \equiv a') = (1/2)F_X = 1/4$$

$$\gamma_{XX'} = P(a \equiv b \equiv b') = (1/2)F_X = 1/4$$

$$\delta_{\bar{X}\bar{X}'} = P(a \equiv b \text{ and } a' \equiv b' \text{ and } a \neq a') = (1/2)F_X F_{X'} = 1/8$$

$$\delta_{\bar{X}+\bar{X}'} = P(a \equiv a' \text{ and } a' \equiv b') = P(a \equiv b' \text{ and } b \equiv a') = (1/2)^2(1 - F_X) = 1/8 \text{ and}$$

$$\delta_{XX'} = P(a \equiv b \equiv a' \equiv b') = (1/2)F_X^2 = (1/2)^2 = 1/8$$

$$\Delta_{\bar{X}\bar{X}'} = P(a \equiv b \text{ and } a' \equiv b') = \delta_{\bar{X}\bar{X}'} + \delta_{XX'} = 1/8 + 1/8 = 1/4$$

The covariance of S_1 relatives from the S_0 family is therefore:

$$C_{XX} = \sigma_A^2 + (1/4)\sigma_D^2 + D_1 + (1/8)D_2$$

This result was given by Cockerham (1983). Extending the covariance to include epistatic variances results in:

$$C_{XX} = \sigma_A^2 + (1/4)\sigma_D^2 + D_1 + (1/8)D_2 + \sigma_{AA}^2 + (1/4)\sigma_{AD}^2 + (1/16)\sigma_{DD}^2 + \dots$$

To derive the covariance of S_1 plants from the same full-sib family but descended from different S_0 plants, we require the identity by descent measures for individuals X and Y in the pedigree:

$$\theta_{XY} = P(a \equiv c) = P(a \equiv d) = P(b \equiv c) = P(b \equiv d) = (1/2)^2 [(2 + F_{P1} + F_{P2})/2]$$

$$\gamma_{\dot{X}Y} = \gamma_{\dot{X}\dot{Y}} = P(a \equiv b \equiv c) = P(a \equiv b \equiv d) = P(a \equiv c)F_X$$

$$\delta_{\dot{X}+\dot{Y}} = P(a \equiv c \text{ and } b \equiv d \text{ and } a \neq b) = (1 - F_X) [P(a \equiv c)]^2$$

$$\delta_{\dot{X}\dot{Y}} = P(a \equiv b \text{ and } c \equiv d \text{ and } a \neq c) = F_X F_Y [1 - P(a \equiv c)]^2$$

$$\delta_{\dot{X}\dot{Y}} = P(a \equiv b \equiv c \equiv d) = F_X F_Y P(a \equiv c)$$

For the IABG1C0 population $F_{P1} = F_{P2} = 0$, such that:

$$\theta_{XY} = 1/4, \gamma_{\dot{X}Y} = 1/8, \delta_{\dot{X}\dot{Y}} = 3/16, \delta_{\dot{X}+\dot{Y}} = 1/32, \delta_{\dot{X}\dot{Y}} = 1/16, \text{ and the covariance of X and Y is :}$$

$$C_{XY} = (1/2)\sigma_A^2 + (1/16)\sigma_D^2 + (1/2)D_1 + (1/16)D_2$$

If the epistatic are included, the covariance of X and Y becomes :

$$C_{XY} = (1/2)\sigma_A^2 + (1/16)\sigma_D^2 + (1/2)D_1 + (1/16)D_2 + (1/4)\sigma_{AA}^2 + (1/32)\sigma_{AD}^2 + (1/256)\sigma_{DD}^2 + \dots$$

For the IABG1C1, IABG2C0, and IABG2C1 populations, $F_{P1} = F_{P2} = 1/2$, so the covariance of S_1 progeny from the same full-sib family but different S_0 parents is derived as:

$\theta_{XY} = 3/8, \gamma_{\bar{X}\bar{Y}} = 3/16, \delta_{\bar{X}\bar{Y}} = 5/32, \delta_{\bar{X}+\bar{Y}} = 9/128, \delta_{\bar{X}\bar{Y}} = 3/32$, and the covariance of X and Y is :

$$C_{XY} = (3/4)\sigma_A^2 + (9/64)\sigma_D^2 + (3/4)D_1 + (3/32)D_2$$

If the epistatic are included, the covariance of X and Y becomes :

$$C_{XY} = (3/4)\sigma_A^2 + (9/64)\sigma_D^2 + (3/4)D_1 + (3/32)D_2 + (9/16)\sigma_{AA}^2 + (27/256)\sigma_{AD}^2 + (81/4096)\sigma_{DD}^2 + \dots$$

The covariance between S_1 progeny from the same S_0 parent is unaffected by the inbreeding coefficient of the parents P_1 and P_2 . For the IABGPI population, one parent is an S_1 plant, and the other is an S_0 , so $F_{P1} = F_{P2} = 1/2$. The resulting covariance of S_1 progeny from the same full-sib family but different S_0 parents is then:

$\theta_{XY} = 5/16, \gamma_{\bar{X}\bar{Y}} = 5/32, \delta_{\bar{X}\bar{Y}} = 5/64, \delta_{\bar{X}+\bar{Y}} = 25/512, \delta_{\bar{X}\bar{Y}} = 5/64$, and the covariance of X

and Y is $C_{XY} = (5/8)\sigma_A^2 + (25/256)\sigma_D^2 + (5/8)D_1 + (5/64)D_2$

If the epistatic are included, the covariance of X and Y becomes :

$$C_{XY} = (5/8)\sigma_A^2 + (25/256)\sigma_D^2 + (5/8)D_1 + (5/64)D_2 + (25/64)\sigma_{AA}^2 + (125/2048)\sigma_{AD}^2 + (625/65536)\sigma_{DD}^2 + \dots$$

For this study, the variances of full sib families and $S_{0:1}$ lines within families of the IABG1C0 population can be written as follows:

$$\begin{aligned}\sigma_{family}^2 = C_{XY} &= (1/2)\sigma_A^2 + (2/32)\sigma_D^2 + (1/2)D_1 + (1/16)D_2 + (1/4)\sigma_{AA}^2 + (1/32)\sigma_{AD}^2 \\ &+ (1/256)\sigma_{DD}^2 \text{ and } \sigma_{line(family)}^2 = C_{XX'} - C_{XY'} = (1/2)\sigma_A^2 + (3/16)\sigma_D^2 + (1/2)D_1 + (1/16)D_2 \\ &+ (3/4)\sigma_{AA}^2 + (7/32)\sigma_{AD}^2 + (15/256)\sigma_{DD}^2\end{aligned}$$

The variance components due to full sib families and $S_{0:1}$ lines of the IABG1C1, IABG2C0 and IABG2C1 populations are:

$$\begin{aligned}\sigma_{family}^2 = C_{XY} &= (3/4)\sigma_A^2 + (9/64)\sigma_D^2 + (3/4)D_1 + (3/32)D_2 + (9/16)\sigma_{AA}^2 + (27/256)\sigma_{AD}^2 \\ &+ (81/4096)\sigma_{DD}^2 \text{ and } \sigma_{line(family)}^2 = C_{XX'} - C_{XY'} = (1/4)\sigma_A^2 + (7/64)\sigma_D^2 + (1/4)D_1 + (1/32)D_2 \\ &+ (7/16)\sigma_{AA}^2 + (37/256)\sigma_{AD}^2 + (175/4096)\sigma_{DD}^2\end{aligned}$$

Under the hypothesis that only additive genetic variance is important, the difference between the variances would fit the following equalities:

$\sigma_{family}^2 - \sigma_{line(family)}^2 = 0$ for IABG1C0 and $\sigma_{family}^2 - 3\sigma_{line(family)}^2 = 0$ for IABG1C1, IABGG2C0 and IABG2C1. These equations led themselves immediately to a statistical test of the hypothesis.

**APPENDIX D. MEAN AGRONOMIC AND GRAIN QUALITY TRAITS OF
EXPERIMENTAL OAT LINES AND CHECK CULTIVARS WITHIN EACH OF
FOUR EVALUATION ENVIRONMENTS**

Table 1. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set one evaluated in 1996 at

Ames, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β -Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
1	IA95196-7	IABG2C1	307.9	965.9	466.2	57.9	196.9	72.7	85.3	90.3
2	IA95196-5	IABG2C1	333.5	1053.2	453.1	63.5	199.0	75.7	86.0	95.3
3	IA95189-9	IABG2C1	87.8	96.1
4	IA95189-2	IABG2C1	239.8	893.4	444.2	69.5	226.8	62.0	88.5	100.2
5	IA95181-6	IABG2C1	88.6	93.7
6	IA95181-4	IABG2C1	229.0	846.4	481.3	70.7	224.0	62.5	87.4	89.4
7	IA95172-4	IABG2C1	88.2	82.8
8	IA95172-1	IABG2C1	301.8	1024.6	481.1	71.2	209.1	74.2	83.4	93.3
9	IA95148-3	IABG2C1	232.6	786.6	470.7	76.5	194.9	64.7	87.7	82.8
10	IA95148-1	IABG2C1	229.5	791.7	435.1	76.6	198.6	61.8	87.6	89.6
11	IA95109-3	IABG2C1	223.2	899.8	452.4	82.0	215.9	54.2	89.8	80.8
12	IA95109-2	IABG2C1	262.7	893.6	468.0	73.8	208.5	65.5	88.0	84.7
13	IA95103-6	IABG2C1	305.6	998.2	475.6	74.3	206.1	66.2	87.7	96.0
14	IA95103-3	IABG2C1	301.9	1051.5	484.9	69.1	224.9	66.9	87.0	97.9
15	IA95038-9	IABG2C1	303.7	1027.7	473.1	69.4	212.7	58.6	87.3	92.6
16	IA95038-7	IABG2C1	282.5	979.0	485.1	72.3	212.1	61.0	86.8	94.4
17	IA95032-9	IABG2C1	265.6	914.9	463.3	70.6	198.4	71.3	84.7	92.3
18	IA95032-6	IABG2C1	257.8	905.4	474.7	64.4	198.2	67.7	87.9	94.7
19	IA95029-4	IABG2C1	245.5	776.4	441.8	69.0	202.2	67.1	88.5	84.0
20	IA95029-3	IABG2C1	271.2	893.7	484.0	70.4	204.9	69.3	87.0	91.5
21	IA94192-7	IABG2C0	352.9	1260.9	478.9	63.9	211.4	69.1	85.9	93.5
22	IA94192-1	IABG2C0	337.0	967.3	495.8	71.1	216.4	71.3	87.6	89.2
23	IA94190-10	IABG2C0	352.2	1108.2	486.0	78.9	191.8	65.2	83.8	90.2
24	IA94190-1	IABG2C0	371.0	1119.9	469.3	74.4	184.8	68.2	84.0	91.1
25	IA94187-5	IABG2C0	259.5	905.2	467.8	60.6	211.1	60.7	87.6	88.6
26	IA94187-10	IABG2C0	358.5	1145.9	479.3	70.3	201.0	66.1	84.0	86.8
27	IA94178-6	IABG2C0	324.7	1129.8	478.2	66.0	195.4	68.4	87.8	95.5
28	IA94178-1	IABG2C0	370.8	1200.4	456.2	71.8	185.4	64.8	87.9	94.1

Table 1. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set one evaluated in 1996 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
29	IA94163-6	IABG2C0	283.4	962.5	454.0	63.8	214.0	57.2	88.2	91.1
30	IA94163-3	IABG2C0	243.4	1029.9	450.4	71.0	212.1	60.0	88.5	90.8
31	IA94143-7	IABG2C0	336.2	1126.0	463.3	58.9	214.3	71.7	86.4	92.0
32	IA94143-4	IABG2C0	368.4	1273.9	465.8	71.6	200.8	69.8	85.1	94.4
33	IA94059-6	IABG2C0	283.8	892.1	444.0	76.4	221.1	66.1	84.9	84.5
34	IA94059-4	IABG2C0	234.2	905.4	454.9	70.3	223.2	67.8	86.8	85.9
35	IA94056-7	IABG2C0	220.6	962.2	442.0	67.7	220.0	59.9	87.0	94.8
36	IA94056-2	IABG2C0	.	.	.	65.1	.	.	88.4	94.0
37	IA94049-5	IABG2C0	292.7	1014.4	440.0	67.0	223.7	63.9	87.1	91.4
38	IA94049-4	IABG2C0	343.1	1122.8	416.4	87.6	204.8	67.1	86.5	88.1
39	IA94031-7	IABG2C0	289.9	1034.1	457.8	69.5	221.9	56.6	86.9	90.6
40	IA94031-6	IABG2C0	287.0	1005.1	472.0	86.6	222.4	56.4	86.8	90.1
41	IA93150-5	IABGPI	325.1	925.8	470.4	62.0	212.8	66.9	86.1	97.9
42	IA93150-1	IABGPI	293.8	1041.4	441.6	65.9	214.2	63.0	84.4	94.2
43	IA93108-5	IABG1C1	261.3	955.0	470.0	68.7	194.5	59.6	87.9	95.5
44	IA93108-4	IABG1C1	279.5	934.0	487.3	67.1	207.2	62.5	87.1	91.4
45	IA93089-4	IABG1C1	411.1	1275.6	478.0	66.3	191.1	58.7	87.9	96.1
46	IA93089-1	IABG1C1	361.1	1237.0	473.6	66.3	196.2	62.6	88.0	98.5
47	IA93067-5	IABGPI	273.3	1004.2	426.0	59.5	202.5	71.4	84.1	98.7
48	IA93067-2	IABGPI	347.9	1135.0	439.1	61.2	199.0	71.6	86.9	95.7
49	IA93061-5	IABGPI	254.1	973.5	429.8	60.4	229.8	70.6	86.3	91.7
50	IA93061-3	IABGPI	264.4	908.9	512.9	49.9	211.1	78.6	87.0	91.6
51	IA93052-6	IABG1C1	237.8	972.9	474.4	67.4	225.2	63.0	87.2	96.6
52	IA93052-5	IABG1C1	87.8	93.7
53	IA93034-2	IABGPI	322.3	1014.2	457.6	69.4	206.6	76.4	82.6	89.0
54	IA93034-1	IABGPI	279.0	981.9	454.0	68.4	217.3	73.6	86.4	90.3
55	IA93029-6	IABG1C1	351.7	1157.8	454.7	81.6	191.6	57.4	85.6	93.4
56	IA93029-4	IABG1C1	359.3	1249.7	468.9	70.9	187.5	67.1	88.4	92.9

Table 1. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set one evaluated in 1996 at

Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β -Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
57	IA93028-3	IABGPI	339.3	1136.3	449.8	62.3	202.4	73.6	87.5	96.9
58	IA93028-2	IABGPI	342.2	1233.7	424.7	57.7	214.8	69.2	83.4	99.7
59	IA93014-3	IABGPI	343.7	1103.6	453.3	65.0	201.1	69.5	86.0	93.2
60	IA93014-1	IABGPI	302.9	1102.7	448.7	66.1	202.6	75.3	87.5	96.1
61	IA91509-4	IABGIC0	322.5	1069.8	423.3	70.0	200.0	64.4	89.1	92.2
62	IA91509-2	IABGIC0	357.3	1168.0	446.4	58.6	204.6	67.0	84.5	96.6
63	IA91504-2	IABGIC0	416.7	1527.0	481.6	60.3	184.9	75.4	89.2	101.3
64	IA91504-11	IABGIC0	398.1	1404.4	444.7	58.1	192.8	71.4	88.8	93.3
65	IA91500-8	IABGIC0	312.5	1417.1	448.2	59.7	194.6	66.0	88.3	104.6
66	IA91500-6	IABGIC0	335.2	1388.7	432.2	54.5	181.2	72.7	87.9	98.5
67	IA91486-2	IABGIC0	320.1	1113.2	469.8	58.9	192.1	61.2	86.9	94.3
68	IA91486-11	IABGIC0	287.4	1156.2	482.4	57.2	202.6	58.0	87.5	96.6
69	IA91485-4	IABGIC0	398.8	1223.4	488.9	59.5	178.8	60.3	88.5	100.1
70	IA91485-18	IABGIC0	256.2	1038.0	493.3	53.2	194.2	58.0	88.7	100.4
71	IA91479-6	IABGIC0	385.2	1314.2	489.6	49.8	191.1	66.0	87.1	101.1
72	IA91479-2	IABGIC0	299.9	1284.1	446.9	49.2	207.4	66.0	88.6	107.5
73	IA91478-6	IABGIC0	301.0	1005.4	492.0	56.5	193.6	68.2	82.9	98.1
74	IA91478-1	IABGIC0	320.8	1100.5	477.6	44.5	189.2	66.8	83.9	95.5
75	IA91470-3	IABGIC0	341.8	1166.9	479.3	58.0	218.8	63.6	87.2	100.6
76	IA91470-10	IABGIC0	386.7	1320.7	462.4	70.6	206.9	60.1	87.6	97.2
77	IA91462-17	IABGIC0	381.0	1489.6	505.1	55.3	208.1	68.6	89.1	98.6
78	IA91462-11	IABGIC0	273.7	961.6	499.8	66.2	200.4	66.2	88.1	96.8
79	IA91448-3	IABGIC0	293.4	1125.0	450.4	57.6	218.9	64.2	86.3	97.3
80	IA91448-1	IABGIC0	290.5	1192.4	463.1	60.1	212.1	62.6	89.1	89.2
81	IL82-2154	Par. line	273.4	1034.4	470.2	56.1	213.2	70.7	87.2	89.7
82	D831-1-571	Par. line	389.9	1204.9	490.0	58.6	199.7	68.3	83.4	92.4
83	OA926-2	Par. line	337.2	1189.7	492.9	56.4	188.1	61.0	85.9	98.9
84	PI412928	Par. line	326.0	1180.3	449.6	63.8	223.3	56.2	86.7	98.8

Table 1. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set one evaluated in 1996 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	PI504593	Par. line	333.5	1046.7	470.0	63.5	186.6	66.2	84.5	80.2
86	Hazel	Check	382.1	1251.8	472.9	56.6	193.5	77.7	86.1	92.3
87	Hazel	Check	326.8	1096.9	479.3	55.4	200.1	74.6	85.6	91.7
88	Starter	Check	365.8	1113.1	525.6	66.0	198.3	63.4	85.2	88.0
89	Starter	Check	331.6	1057.5	492.0	62.4	197.0	65.8	85.6	93.8
90	Premier	Check	392.3	1284.3	506.0	68.2	179.7	63.7	87.7	93.6
91	Premier	Check	344.6	1134.6	514.2	67.5	186.7	63.0	87.0	93.3
92	Marion	Check	428.9	1397.3	482.0	63.2	181.1	74.9	86.9	105.0
93	Marion	Check	374.1	1264.9	483.3	61.4	183.5	74.6	87.8	104.7
94	Noble	Check	370.3	1306.2	478.2	46.7	204.7	63.0	86.8	91.8
95	Noble	Check	306.8	1021.9	495.8	52.5	204.7	62.8	86.6	95.1
96	Ogle	Check	363.0	1347.3	438.0	52.0	199.2	59.7	86.7	96.1
97	Ogle	Check	337.7	1322.0	441.8	53.1	202.9	59.7	88.2	95.3
98	Don	Check	338.3	1016.4	445.1	45.4	162.2	75.6	83.7	88.2
99	Don	Check	348.3	1062.2	482.9	50.2	167.6	75.5	83.9	86.1
100	IAN979-5-2	Check	309.7	1078.5	442.0	72.2	208.2	74.2	89.9	87.9
Mean [†]			310.8	1118.0	495.9	57.0	193.0	67.5	86.7	93.5
LSD [‡]	Entry vs Entry		164.1	397.1	63.0	9.6	12.1	3.5	3.9	7.3

[†] Mean of all entries evaluated in 1996 at Ames.

[‡] Least significant difference at the 0.05 probability level.

Table 2. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set two evaluated in 1996 at

Ames, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
1	IA95196-7	IABG2C1	228.2	799.6	544.4	77.1	214.2	64.5	87.0	88.5
2	IA95196-5	IABG2C1	194.1	825.4	428.9	70.9	209.1	66.8	88.2	89.2
3	IA95189-9	IABG2C1	162.8	694.0	450.4	81.9	216.9	52.8	86.2	86.4
4	IA95189-2	IABG2C1	167.3	629.2	454.4	79.3	206.4	57.3	85.3	92.3
5	IA95181-6	IABG2C1	89.8	79.6
6	IA95181-4	IABG2C1	87.8	84.5
7	IA95172-4	IABG2C1	187.9	688.9	458.4	80.4	198.2	52.9	85.3	89.9
8	IA95172-1	IABG2C1	87.0	87.9
9	IA95148-3	IABG2C1	311.5	1042.6	463.3	65.2	201.7	78.7	82.9	94.6
10	IA95148-1	IABG2C1	207.6	911.1	437.3	68.9	217.8	77.7	87.4	93.9
11	IA95109-3	IABG2C1	330.4	1166.1	428.4	71.9	192.6	59.5	88.6	106.6
12	IA95109-2	IABG2C1	262.8	965.2	447.8	66.0	207.3	64.5	87.0	97.3
13	IA95103-6	IABG2C1	90.2	83.2
14	IA95103-3	IABG2C1	250.4	898.4	478.4	64.4	206.9	55.9	85.3	90.4
15	IA95038-9	IABG2C1	238.5	853.2	460.7	67.0	213.4	61.7	86.2	90.9
16	IA95038-7	IABG2C1	197.5	775.3	420.0	67.3	229.0	57.7	88.2	94.5
17	IA95032-9	IABG2C1	176.5	672.5	435.6	68.5	207.9	63.7	88.2	86.3
18	IA95032-6	IABG2C1	265.3	805.2	449.3	74.1	208.5	61.2	85.3	81.0
19	IA95029-4	IABG2C1	261.6	881.0	496.9	71.2	191.1	69.4	87.4	92.0
20	IA95029-3	IABG2C1	264.2	1023.8	493.6	73.2	186.5	63.2	87.4	91.1
21	IA94192-7	IABG2C0	383.1	1422.6	489.6	67.0	206.7	69.5	88.6	97.4
22	IA94192-1	IABG2C0	348.9	1356.2	483.6	70.5	204.6	66.6	89.0	96.4
23	IA94190-10	IABG2C0	368.6	1182.6	461.1	71.7	200.4	60.4	85.3	84.2
24	IA94190-1	IABG2C0	466.4	1459.4	489.8	66.9	209.0	62.5	87.0	82.3
25	IA94187-5	IABG2C0	401.1	1186.4	445.1	61.4	199.8	74.6	79.6	92.0
26	IA94187-10	IABG2C0	255.2	1029.5	457.1	59.8	234.7	70.6	81.3	100.3
27	IA94178-6	IABG2C0	229.6	843.3	490.7	80.6	219.7	52.5	83.3	89.0
28	IA94178-1	IABG2C0	224.4	877.4	488.2	75.0	224.5	42.6	82.5	80.2

Table 2. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set two evaluated in 1996 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m^{-2}	Biomass g m^{-2}	Test weight kg m^{-3}	β -Glucan content g kg^{-1}	Protein content g kg^{-1}	Oil content g kg^{-1}	Heading date dap	Height cm
29	IA94163-6	IABG2C0	338.9	1108.5	478.9	67.0	198.8	70.1	87.0	87.4
30	IA94163-3	IABG2C0	439.8	1319.5	487.6	62.0	199.9	71.5	86.6	85.2
31	IA94143-7	IABG2C0	88.2	84.0
32	IA94143-4	IABG2C0	289.9	1114.9	478.0	78.6	215.6	63.2	86.6	93.6
33	IA94059-6	IABG2C0	313.1	1136.0	483.6	70.5	204.6	67.0	87.0	94.3
34	IA94059-4	IABG2C0	397.9	1236.6	486.4	73.7	194.8	62.4	84.9	94.3
35	IA94056-7	IABG2C0	201.5	846.9	460.2	69.7	224.6	58.8	88.2	91.1
36	IA94056-2	IABG2C0	89.0	85.9
37	IA94049-5	IABG2C0	420.7	1416.7	494.0	55.5	198.7	67.7	84.5	99.5
38	IA94049-4	IABG2C0	247.0	1214.4	511.6	64.8	198.4	60.1	85.3	99.0
39	IA94031-7	IABG2C0	87.8	73.2
40	IA94031-6	IABG2C0	224.8	804.9	476.7	68.7	205.2	63.4	84.5	78.1
41	IA93150-5	IABG1C1	402.9	1389.6	494.4	64.2	219.5	56.6	84.9	93.8
42	IA93150-1	IABG1C1	324.1	1218.7	528.7	67.3	220.1	58.3	85.3	99.8
43	IA93108-5	IABG1C1	336.3	1172.3	501.6	62.3	218.5	59.3	84.1	90.1
44	IA93108-4	IABG1C1	301.0	1171.8	460.4	68.9	215.0	54.2	87.0	87.5
45	IA93089-4	IABG1C1	510.6	1730.9	463.3	64.9	200.3	63.5	89.4	93.1
46	IA93089-1	IABG1C1	365.5	1348.6	479.6	70.3	199.6	58.3	91.5	94.4
47	IA93067-5	IABG1C1	357.3	1405.4	497.8	67.6	212.4	66.5	87.4	93.6
48	IA93067-2	IABG1C1	344.7	1304.2	493.3	68.6	218.3	65.8	88.6	104.0
49	IA93061-5	IABG1C1	291.5	1116.8	471.8	56.3	191.3	61.7	87.8	90.4
50	IA93061-3	IABG1C1	363.6	1385.0	485.1	56.1	205.1	60.9	87.8	96.5
51	IA93052-6	IABG1C1	258.9	1010.3	451.8	61.8	196.4	71.6	85.3	91.9
52	IA93052-5	IABG1C1	262.8	872.5	488.9	61.6	207.2	72.0	83.3	90.1
53	IA93034-2	IABG1C1	395.0	1600.6	456.2	64.1	206.5	68.6	89.4	96.2
54	IA93034-1	IABG1C1	413.7	1318.6	476.0	62.3	209.6	65.4	86.2	89.8
55	IA93029-6	IABG1C1	177.5	906.4	443.6	61.8	234.4	56.6	84.1	86.9
56	IA93029-4	IABG1C1	261.0	987.0	467.8	59.5	227.3	58.8	83.7	86.5

Ames, IA (continued).

[illegible]

Table 2. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set two evaluated in 1996 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	PI504601	Par. line	305.3	1167.5	514.0	51.1	211.7	68.6	84.5	91.4
86	Hazel	Check	371.9	1202.7	474.2	57.1	199.9	76.2	84.5	91.4
87	Hazel	Check	368.1	1188.6	502.4	56.3	201.1	77.3	84.9	87.8
88	Starter	Check	335.6	1123.3	510.9	59.0	196.9	66.0	83.7	92.4
89	Starter	Check	332.6	1089.7	502.7	56.6	199.3	65.6	84.1	89.3
90	Premier	Check	355.7	1263.3	540.0	65.2	193.4	63.1	87.4	93.9
91	Premier	Check	321.6	1126.0	516.2	68.6	197.7	63.0	88.2	92.3
92	Marion	Check	284.8	1058.3	460.0	76.4	187.9	72.5	88.6	103.8
93	Marion	Check	389.5	1221.6	495.1	67.3	184.5	71.6	86.6	102.3
94	Noble	Check	331.7	1294.5	483.6	50.3	213.7	59.8	86.2	93.0
95	Noble	Check	270.0	1047.2	514.0	51.2	218.5	59.5	87.0	93.2
96	Ogle	Check	397.1	1581.8	456.7	54.6	201.2	59.0	87.4	96.4
97	Ogle	Check	345.9	1406.6	463.6	48.9	204.9	58.8	86.2	98.1
98	Don	Check	312.1	983.3	486.2	49.5	176.1	72.6	83.3	87.6
99	Don	Check	289.0	917.8	488.9	51.5	171.9	72.3	82.5	84.8
100	IAN979-5-2	Check	307.7	1191.2	448.0	81.2	210.4	71.7	89.0	89.3
Mean [†]			310.8	1118.0	495.9	57.0	193.0	67.5	86.7	93.5
LSD [‡]	Entry vs Entry		164.1	397.1	63.02	9.6	12.1	3.5	3.9	7.3

[†] Mean of all entries evaluated in 1996 at Ames.

[‡] Least significant difference at the 0.05 probability level.

Table 3. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set three evaluated in 1996 at

Ames, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
1	IA95196-7	IABG2C1	129.0	523.8	440.9	81.2	222.9	55.1	88.4	86.4
2	IA95196-5	IABG2C1	138.3	571.4	478.4	84.6	226.0	56.1	88.4	80.3
3	IA95189-9	IABG2C1	338.9	892.7	489.8	60.6	204.3	76.3	86.1	99.2
4	IA95189-2	IABG2C1	300.0	1147.6	475.6	61.6	219.0	64.9	81.6	92.8
5	IA95181-6	IABG2C1	272.8	1028.5	458.0	65.0	225.9	65.4	88.2	103.2
6	IA95181-4	IABG2C1	241.7	884.6	514.7	62.7	220.1	63.7	83.7	93.3
7	IA95172-4	IABG2C1	179.5	897.2	448.4	69.1	210.1	56.9	84.9	84.8
8	IA95172-1	IABG2C1	218.4	837.4	486.0	75.6	209.1	59.2	86.2	80.2
9	IA95148-3	IABG2C1	191.2	864.1	388.9	66.4	216.9	58.2	89.0	95.0
10	IA95148-1	IABG2C1	265.0	1150.2	520.9	72.6	210.2	62.7	87.4	94.0
11	IA95109-3	IABG2C1	245.6	966.7	450.4	78.3	208.6	67.7	88.5	86.4
12	IA95109-2	IABG2C1	233.9	916.9	446.2	77.9	212.1	65.4	86.6	93.4
13	IA95103-6	IABG2C1	222.3	820.7	476.9	82.3	218.8	52.4	86.0	84.2
14	IA95103-3	IABG2C1	230.0	831.6	440.7	78.0	209.9	60.5	87.0	91.9
15	IA95038-9	IABG2C1	179.5	844.4	440.4	74.9	230.8	58.4	88.7	84.7
16	IA95038-7	IABG2C1	89.3	77.9
17	IA95032-9	IABG2C1	148.4	627.8	460.7	69.2	214.5	60.5	90.6	98.2
18	IA95032-6	IABG2C1	85.4	93.7
19	IA95029-4	IABG2C1	85.9	83.3
20	IA95029-3	IABG2C1	233.9	893.0	406.9	68.0	211.5	63.6	87.4	90.9
21	IA94192-7	IABG2C0	280.6	1043.1	494.0	65.7	216.0	66.0	85.4	89.0
22	IA94192-1	IABG2C0	280.6	989.7	469.6	61.3	215.3	67.6	85.9	88.4
23	IA94190-10	IABG2C0	82.7	87.0
24	IA94190-1	IABG2C0	83.1	83.2
25	IA94187-5	IABG2C0	366.1	1473.4	517.8	64.0	217.3	68.5	87.7	97.5
26	IA94187-10	IABG2C0	350.5	1480.5	472.9	67.4	216.4	68.1	87.6	100.4
27	IA94178-6	IABG2C0	222.3	902.6	476.4	73.2	204.9	53.0	85.0	85.5
28	IA94178-1	IABG2C0	268.9	969.7	490.9	78.4	213.3	51.6	87.5	82.6

Table 3. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set three evaluated in 1996 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
29	IA94163-6	IABG2C0	140.6	739.3	464.9	64.1	244.4	45.4	86.3	84.8
30	IA94163-3	IABG2C0	218.4	917.4	534.2	77.4	223.3	52.7	87.0	96.2
31	IA94143-7	IABG2C0	346.6	1215.3	443.1	60.2	209.5	58.2	88.9	90.4
32	IA94143-4	IABG2C0	268.9	1141.8	504.0	62.6	223.1	58.9	86.6	97.8
33	IA94059-6	IABG2C0	241.7	913.8	476.0	53.9	211.2	61.4	89.2	87.8
34	IA94059-4	IABG2C0	272.8	1164.6	606.9	63.0	212.8	61.4	88.2	90.8
35	IA94056-7	IABG2C0	206.7	806.0	502.7	78.4	199.6	58.6	84.4	94.9
36	IA94056-2	IABG2C0	87.3	97.9
37	IA94049-5	IABG2C0	276.7	998.9	514.4	78.0	199.6	61.6	87.7	89.4
38	IA94049-4	IABG2C0	257.2	900.7	481.1	83.6	201.2	59.0	86.6	89.6
39	IA94031-7	IABG2C0	370.0	1158.5	449.1	68.6	197.7	62.0	86.0	84.1
40	IA94031-6	IABG2C0	494.3	1470.9	419.1	78.7	199.2	64.2	84.9	88.9
41	IA93150-5	IABG1C1	385.5	1522.9	472.0	66.4	218.1	65.8	87.9	95.4
42	IA93150-1	IABG1C1	237.8	1005.1	440.4	69.8	216.6	66.6	88.5	97.7
43	IA93108-5	IABGPI	88.3	92.3
44	IA93108-4	IABGPI	404.9	1313.3	459.8	60.7	223.1	69.7	83.9	91.5
45	IA93089-4	IABGPI	377.7	1183.7	476.0	63.7	195.8	73.5	84.3	101.5
46	IA93089-1	IABGPI	408.8	1433.5	447.3	66.9	196.4	66.3	86.6	100.6
47	IA93067-5	IABG1C1	311.7	1149.1	444.7	61.2	218.0	64.0	89.9	92.3
48	IA93067-2	IABG1C1	272.8	890.1	465.3	63.3	215.0	58.7	84.6	82.0
49	IA93061-5	IABG1C1	346.6	1218.7	467.8	60.8	219.1	69.1	86.9	94.4
50	IA93061-3	IABG1C1	362.2	1216.7	488.2	64.1	217.1	68.1	88.0	94.4
51	IA93052-6	IABG1C1	249.5	913.4	454.4	72.6	208.3	68.4	84.6	87.7
52	IA93052-5	IABG1C1	307.8	1253.4	479.8	69.2	201.9	67.1	87.7	95.6
53	IA93034-2	IABG1C1	451.6	1438.1	504.7	72.4	198.4	73.5	86.9	89.4
54	IA93034-1	IABG1C1	358.3	1164.7	509.6	78.5	211.1	67.7	83.0	88.9
55	IA93029-6	IABGPI	498.2	1680.8	487.8	69.0	195.1	70.9	90.1	110.0
56	IA93029-4	IABGPI	276.7	1197.0	495.6	58.4	201.4	65.8	87.6	107.3

Table 3. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set three evaluated in 1996 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
57	IA93028-3	IABGPI	245.6	1012.7	488.9	56.8	216.8	74.2	84.4	98.8
58	IA93028-2	IABGPI	296.1	1258.7	482.4	67.9	221.1	74.6	89.0	99.8
59	IA93014-3	IABG1C1	397.2	1549.1	527.1	65.1	204.6	65.4	88.3	98.8
60	IA93014-1	IABG1C1	89.2	93.2
61	IA91509-4	IABG1C0	335.0	1099.6	478.7	61.9	204.4	72.5	85.4	91.0
62	IA91509-2	IABG1C0	393.3	1343.1	481.3	59.3	212.8	75.6	87.4	100.3
63	IA91504-2	IABG1C0	175.6	778.1	454.2	55.4	208.1	67.6	86.2	88.4
64	IA91504-11	IABG1C0	381.6	1227.0	528.2	53.1	194.7	57.9	87.1	96.3
65	IA91500-8	IABG1C0	245.6	1023.0	476.7	58.4	211.2	63.6	86.8	96.7
66	IA91500-6	IABG1C0	292.2	1400.4	477.8	63.7	215.5	57.8	89.0	98.4
67	IA91486-2	IABG1C0	416.6	1337.7	489.1	54.1	194.6	65.0	86.9	103.8
68	IA91486-11	IABG1C0	350.5	1391.6	453.3	50.4	214.3	68.4	85.2	106.2
69	IA91485-4	IABG1C0	296.1	1036.0	477.3	60.1	202.1	68.2	87.1	98.0
70	IA91485-18	IABG1C0	315.5	1265.1	481.8	57.2	195.2	69.8	90.8	98.0
71	IA91479-6	IABG1C0	307.8	1322.4	498.9	50.3	205.1	61.8	91.0	106.5
72	IA91479-2	IABG1C0	319.4	1268.8	502.9	49.3	207.7	64.6	86.8	98.2
73	IA91478-6	IABG1C0	420.5	1742.4	512.2	63.0	207.4	63.4	89.2	102.6
74	IA91478-1	IABG1C0	412.7	1530.4	453.3	57.0	210.5	64.4	88.9	100.8
75	IA91470-3	IABG1C0	338.9	1049.2	471.3	61.2	220.9	65.7	85.5	95.1
76	IA91470-10	IABG1C0	86.3	98.0
77	IA91462-17	IABG1C0	338.9	1459.3	469.6	63.7	217.9	72.4	88.5	92.1
78	IA91462-11	IABG1C0	303.9	1028.8	504.9	58.8	203.7	69.1	83.5	90.1
79	IA91448-3	IABG1C0	478.8	1636.6	491.3	57.3	212.7	55.9	87.5	104.3
80	IA91448-1	IABG1C0	498.2	1733.0	456.9	58.3	201.7	61.9	90.6	105.4
81	H87-7-4	Par. line	87.7	95.8
82	MO07929	Par. line	358.3	1262.4	467.1	53.4	214.7	75.7	87.0	96.9
83	MN88156	Par. line	284.4	1000.6	477.1	62.3	212.7	56.0	85.7	92.3
84	NO4-8	Par. line	272.8	1223.5	476.9	53.0	216.6	61.9	87.7	106.5

Table 3. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set three evaluated in 1996 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	PI361884	Par. line	455.5	1415.5	496.2	53.8	187.3	66.6	86.5	99.0
86	Hazel	Check	338.9	1205.2	470.4	52.4	202.9	74.8	85.2	86.4
87	Hazel	Check	257.2	1022.1	480.7	49.9	205.6	74.9	86.5	87.1
88	Starter	Check	370.0	1126.3	530.0	55.2	199.9	61.5	84.8	90.3
89	Starter	Check	303.9	1096.9	456.7	52.2	204.2	63.3	85.9	96.9
90	Premier	Check	401.0	1301.9	493.8	66.3	192.8	60.6	86.1	95.7
91	Premier	Check	389.4	1373.1	507.3	62.4	188.3	63.8	87.0	97.9
92	Marion	Check	521.5	1635.5	460.0	59.6	179.6	74.4	86.1	107.1
93	Marion	Check	436.0	1466.3	435.3	64.1	190.8	74.0	87.6	102.4
94	Noble	Check	268.3	1062.2	467.8	47.0	215.0	60.7	86.4	94.8
95	Noble	Check	288.3	1151.6	468.2	53.2	212.5	60.2	86.8	91.2
96	Ogle	Check	428.3	1689.1	483.8	47.5	194.4	60.1	87.4	98.0
97	Ogle	Check	346.6	1343.0	444.2	54.2	201.4	58.0	86.7	95.8
98	Don	Check	284.4	883.7	493.6	43.7	168.0	73.2	84.7	86.5
99	Don	Check	303.9	1012.7	482.0	44.4	168.7	73.5	83.5	88.2
100	IAN979-5-2	Check	412.7	1454.9	474.2	55.2	193.8	50.6	88.3	88.8
Mean [†]			310.8	1118.0	495.9	57.0	193.0	67.5	86.7	93.5
LSD [‡]	Entry vs Entry		164.1	397.1	63.0	9.6	12.1	3.5	3.9	7.3

[†] Mean of all entries evaluated in 1996 at Ames.

[‡] Least significant difference at the 0.05 probability level.

Table 4. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set four evaluated in 1996 at

Ames, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β -Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
1	IA95196-7	IABG2C1	164.8	629.8	473.6	57.5	180.0	71.4	87.4	92.3
2	IA95196-5	IABG2C1	157.4	703.3	488.9	67.1	210.2	61.5	87.4	88.5
3	IA95189-9	IABG2C1	102.2	617.9	495.6	64.4	230.7	65.4	87.0	83.9
4	IA95189-2	IABG2C1	130.1	686.0	483.6	68.9	241.5	65.2	88.6	90.2
5	IA95181-6	IABG2C1	173.8	561.0	519.3	76.3	222.0	62.0	85.8	83.2
6	IA95181-4	IABG2C1	112.6	1079.9	491.6	71.5	243.3	57.9	87.0	87.7
7	IA95172-4	IABG2C1	87.9	698.5	471.3	65.9	224.2	59.0	89.7	95.0
8	IA95172-1	IABG2C1	247.7	1046.8	488.9	75.8	216.2	69.8	89.0	101.1
9	IA95148-3	IABG2C1	264.8	970.5	493.1	69.7	207.4	70.0	87.8	96.4
10	IA95148-1	IABG2C1	251.3	964.1	499.3	68.3	207.4	69.1	89.4	99.3
11	IA95109-3	IABG2C1	89.0	82.2
12	IA95109-2	IABG2C1	115.3	657.0	521.3	73.4	209.7	67.9	90.5	93.2
13	IA95103-6	IABG2C1	173.1	774.8	422.7	61.9	209.2	64.9	90.5	90.1
14	IA95103-3	IABG2C1	219.5	905.0	498.7	66.4	204.1	69.3	88.2	91.6
15	IA95038-9	IABG2C1	183.3	739.2	508.4	71.2	209.0	60.4	89.0	90.4
16	IA95038-7	IABG2C1	168.5	749.3	418.0	81.8	214.9	62.5	91.3	90.0
17	IA95032-9	IABG2C1	133.4	645.4	507.1	79.4	202.6	66.9	88.6	83.5
18	IA95032-6	IABG2C1	130.1	681.8	491.3	84.8	214.5	60.5	87.8	81.4
19	IA95029-4	IABG2C1	95.7	669.8	490.4	79.5	256.2	55.7	88.6	86.7
20	IA95029-3	IABG2C1	154.7	711.3	507.8	85.3	236.4	52.1	87.4	78.5
21	IA94192-7	IABG2C0	234.4	827.2	507.8	75.0	212.8	67.5	84.3	84.1
22	IA94192-1	IABG2C0	299.6	1018.8	500.9	71.3	200.0	72.6	86.6	89.9
23	IA94190-10	IABG2C0	81.5	91.3
24	IA94190-1	IABG2C0	216.0	983.0	503.3	74.2	225.5	51.8	84.6	90.5
25	IA94187-5	IABG2C0	408.1	1218.8	542.7	63.9	207.5	73.7	83.9	90.5
26	IA94187-10	IABG2C0	373.8	1222.0	449.3	63.6	194.8	72.4	87.0	87.8
27	IA94178-6	IABG2C0	328.1	1004.7	481.1	70.5	202.4	68.4	84.3	85.2
28	IA94178-1	IABG2C0	481.6	1256.5	463.8	65.2	197.9	75.7	87.4	92.2

Table 4. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set four evaluated in 1996 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
29	IA94163-6	IABG2C0	325.9	1033.6	507.1	61.0	188.5	70.2	85.8	88.4
30	IA94163-3	IABG2C0	439.7	1240.0	425.8	60.3	199.8	71.5	84.3	91.4
31	IA94143-7	IABG2C0	207.1	943.4	471.8	69.7	217.7	53.4	83.1	91.9
32	IA94143-4	IABG2C0	88.2	90.5
33	IA94059-6	IABG2C0	276.4	989.5	475.1	72.3	198.7	65.1	84.6	90.3
34	IA94059-4	IABG2C0	231.4	1030.6	458.9	75.9	224.1	61.2	84.6	91.1
35	IA94056-7	IABG2C0	217.0	886.6	509.6	69.1	227.9	57.3	87.4	90.2
36	IA94056-2	IABG2C0	200.9	956.0	463.3	64.8	236.8	56.8	90.1	90.6
37	IA94049-5	IABG2C0	171.3	976.3	491.1	54.7	239.6	60.9	83.5	95.5
38	IA94049-4	IABG2C0	218.6	1245.7	512.4	52.4	223.1	65.6	87.0	98.9
39	IA94031-7	IABG2C0	287.6	1181.4	484.9	61.2	220.6	60.5	87.8	90.2
40	IA94031-6	IABG2C0	296.1	1273.0	424.0	62.4	209.8	62.7	87.4	93.6
41	IA93150-5	IABGPI	444.2	1348.5	541.1	59.0	185.9	74.6	92.1	103.1
42	IA93150-1	IABGPI	234.3	952.1	473.6	59.9	203.8	74.1	89.7	105.3
43	IA93108-5	IABG1C1	512.0	1450.7	473.1	55.5	207.9	69.3	86.2	97.6
44	IA93108-4	IABG1C1	356.0	1215.8	536.9	62.5	205.1	79.6	86.6	94.5
45	IA93089-4	IABG1C1	269.1	1200.7	473.6	70.2	230.0	59.2	88.6	103.8
46	IA93089-1	IABG1C1	379.6	1167.0	544.7	59.9	207.8	65.4	86.6	98.3
47	IA93067-5	IABGPI	340.3	1099.5	463.3	60.5	198.7	76.0	86.2	88.7
48	IA93067-2	IABGPI	315.9	1015.7	470.9	68.2	189.4	70.5	85.0	90.8
49	IA93061-5	IABGPI	229.3	967.6	500.7	59.2	187.2	75.3	82.7	89.1
50	IA93061-3	IABGPI	414.0	1117.9	457.1	59.1	196.5	76.7	84.3	96.1
51	IA93052-6	IABG1C1	318.1	1090.0	475.6	68.1	199.1	66.5	87.8	94.4
52	IA93052-5	IABG1C1	326.1	1138.5	483.6	72.3	213.1	64.3	88.2	100.4
53	IA93034-2	IABG1C1	260.7	1097.1	463.8	67.0	220.4	65.0	87.0	89.8
54	IA93034-1	IABG1C1	307.1	1078.0	480.4	74.8	225.0	62.3	86.2	84.1
55	IA93029-6	IABG1C1	87.8	103.3
56	IA93029-4	IABG1C1	527.6	1585.6	432.9	63.2	203.9	67.4	88.2	102.7

Table 4. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set four evaluated in 1996 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date day	Height cm
57	IA93028-3	IABGPI	85.4	92.3
58	IA93028-2	IABGPI	189.4	1227.3	460.2	68.4	220.3	60.7	87.0	89.2
59	IA93014-3	IABGIC1	267.0	946.6	472.0	58.2	208.0	66.9	83.9	92.2
60	IA93014-1	IABGIC1	294.5	1011.9	510.2	61.1	213.3	62.4	85.0	87.8
61	IA91509-4	IABGIC0	384.8	1300.0	442.7	62.4	196.1	62.5	88.6	87.8
62	IA91509-2	IABGIC0	85.8	92.4
63	IA91504-2	IABGIC0	314.0	1121.2	493.1	59.5	208.3	62.6	87.4	103.6
64	IA91504-11	IABGIC0	463.5	1499.3	554.2	54.0	185.1	63.8	88.2	100.3
65	IA91500-8	IABGIC0	319.4	1300.9	407.8	56.4	199.2	69.3	87.4	95.8
66	IA91500-6	IABGIC0	88.2	101.3
67	IA91486-2	IABGIC0	281.9	1150.8	495.6	54.0	178.4	69.2	89.4	102.3
68	IA91486-11	IABGIC0	458.4	1127.3	457.1	57.7	181.4	63.0	88.2	99.1
69	IA91485-4	IABGIC0	339.4	1405.0	527.6	56.7	193.1	60.0	88.2	102.7
70	IA91485-18	IABGIC0	426.7	1412.7	521.1	52.1	172.9	66.0	90.5	105.6
71	IA91479-6	IABGIC0	362.8	1193.5	464.0	64.4	202.3	60.6	87.8	97.9
72	IA91479-2	IABGIC0	374.7	1232.8	487.8	53.5	197.4	72.0	87.0	94.0
73	IA91478-6	IABGIC0	393.6	1249.2	459.8	65.7	202.4	66.5	87.8	92.5
74	IA91478-1	IABGIC0	261.1	980.9	619.8	55.0	188.5	66.4	88.2	92.0
75	IA91470-3	IABGIC0	297.8	991.8	482.9	53.7	209.8	62.4	86.6	98.4
76	IA91470-10	IABGIC0	383.2	1193.0	465.1	66.3	205.2	58.7	86.6	91.2
77	IA91462-17	IABGIC0	376.5	1243.4	491.3	59.3	200.2	63.6	85.4	92.6
78	IA91462-11	IABGIC0	86.6	89.9
79	IA91448-3	IABGIC0	291.7	943.4	475.8	63.3	194.0	62.3	85.4	98.4
80	IA91448-1	IABGIC0	517.2	1555.3	516.2	61.4	197.4	69.6	89.4	98.3
81	H730-12	Par. line	143.8	774.6	462.4	65.3	212.2	58.4	89.0	94.7
82	MN86226	Par. line	296.5	1158.1	455.8	68.9	214.5	61.2	89.0	99.4
83	NO20-1	Par. line	87.0	111.1
84	PI361886	Par. line	442.6	1323.2	479.6	67.2	185.4	76.1	92.5	115.2

Table 4. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set four evaluated in 1996 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	PI502955	Par. line	243.9	924.5	496.2	65.5	204.4	71.3	79.2	97.6
86	Hazel	Check	86.6	87.8
87	Hazel	Check	.	.	500.7	51.6	194.9	76.5	83.5	88.8
88	Starter	Check	345.3	1082.4	455.1	56.0	183.0	67.0	84.3	86.1
89	Starter	Check	320.9	970.0	517.6	60.2	195.4	64.4	83.9	87.6
90	Premier	Check	331.1	1134.1	457.8	70.4	202.0	60.6	87.4	92.4
91	Premier	Check	354.7	1094.7	511.8	60.5	195.8	63.1	87.8	95.5
92	Marion	Check	438.8	1276.0	529.8	62.0	185.6	72.7	89.0	102.2
93	Marion	Check	393.0	1159.2	459.8	62.0	180.4	75.3	87.4	105.2
94	Noble	Check	325.4	1231.8	494.7	49.5	214.0	59.6	87.8	92.9
95	Noble	Check	285.8	1024.6	498.7	46.5	208.4	62.1	86.6	97.0
96	Ogle	Check	399.8	1331.2	465.1	50.6	192.3	57.8	86.2	91.9
97	Ogle	Check	411.1	1277.8	500.7	53.0	198.0	60.9	86.2	97.0
98	Don	Check	370.3	1059.6	474.9	51.4	170.2	73.9	82.7	88.1
99	Don	Check	327.6	982.9	494.0	45.2	167.0	75.8	83.1	85.8
100	IAN979-5-2	Check	422.2	1374.9	480.4	72.0	204.9	76.2	90.5	88.6
Mean [†]			310.8	1118.0	495.9	57.0	193.0	67.5	86.7	93.5
LSD [‡]	Entry vs Entry		164.1	397.1	63.0	9.6	12.1	3.5	3.9	7.3

[†] Mean of all entries evaluated in 1996 at Ames.

[‡] Least significant difference at the 0.05 probability level.

Table 5. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set five evaluated in 1996 at Ames, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
1	IA95196-7	IABG2C1	289.4	968.9	496.9	76.0	197.9	72.5	81.6	94.0
2	IA95196-5	IABG2C1	225.9	803.7	506.9	78.4	218.9	68.8	86.0	87.8
3	IA95189-9	IABG2C1	284.5	1105.6	495.6	72.6	218.4	66.1	90.2	91.3
4	IA95189-2	IABG2C1	326.5	1106.3	542.7	76.7	196.3	64.4	87.3	87.8
5	IA95181-6	IABG2C1	247.5	949.1	493.3	66.8	219.0	69.7	85.0	96.6
6	IA95181-4	IABG2C1	273.5	1131.1	517.8	74.9	217.6	67.0	86.7	96.6
7	IA95172-4	IABG2C1	85.4	87.7
8	IA95172-1	IABG2C1	88.8	90.4
9	IA95148-3	IABG2C1	253.7	906.6	508.7	70.3	214.7	68.3	87.7	93.1
10	IA95148-1	IABG2C1	232.7	816.0	469.3	72.7	198.2	59.7	93.2	92.2
11	IA95109-3	IABG2C1	88.2	90.4
12	IA95109-2	IABG2C1	247.8	884.8	494.2	73.3	208.4	66.4	86.5	93.1
13	IA95103-6	IABG2C1	213.4	848.9	424.9	92.2	224.3	58.8	91.2	89.6
14	IA95103-3	IABG2C1	236.1	903.2	460.0	90.1	223.8	61.5	90.7	86.9
15	IA95038-9	IABG2C1	239.1	925.1	498.2	70.5	210.6	77.6	87.3	92.2
16	IA95038-7	IABG2C1	248.2	1049.1	465.1	69.2	227.4	72.1	88.6	92.2
17	IA95032-9	IABG2C1	292.3	978.5	496.2	77.4	197.4	67.4	84.9	94.9
18	IA95032-6	IABG2C1	364.5	1192.0	505.1	79.6	204.8	69.2	84.6	101.1
19	IA95029-4	IABG2C1	88.5	78.1
20	IA95029-3	IABG2C1	211.1	747.9	468.0	81.9	208.4	59.3	88.6	86.0
21	IA94192-7	IABG2C0	325.7	1112.8	510.0	80.3	207.3	58.7	82.0	91.3
22	IA94192-1	IABG2C0	321.2	1054.2	562.4	77.4	211.4	65.3	81.0	91.3
23	IA94190-10	IABG2C0	275.0	967.4	472.4	67.4	204.2	76.9	81.5	90.4
24	IA94190-1	IABG2C0	349.3	1206.5	477.1	66.4	214.9	77.4	79.4	94.9
25	IA94187-5	IABG2C0	263.6	1168.8	467.3	81.2	211.1	61.1	89.4	94.9
26	IA94187-10	IABG2C0	229.6	1009.1	447.6	77.8	220.8	57.6	88.5	89.6
27	IA94178-6	IABG2C0	325.0	1077.9	528.7	85.7	218.8	61.2	84.3	89.6
28	IA94178-1	IABG2C0	261.2	981.1	520.7	79.4	214.8	64.8	86.5	89.6

Table 5. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set five evaluated in 1996 at

Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
29	IA94163-6	IABG2C0	297.5	1060.6	535.8	76.4	203.1	68.1	84.9	94.0
30	IA94163-3	IABG2C0	337.3	1194.7	523.8	73.6	194.8	75.1	86.6	92.2
31	IA94143-7	IABG2C0	286.9	1140.4	533.1	72.6	217.0	62.0	85.8	94.0
32	IA94143-4	IABG2C0	276.3	1008.0	542.7	64.8	203.5	62.5	86.1	92.2
33	IA94059-6	IABG2C0	254.9	877.3	502.4	77.2	228.5	57.1	82.6	71.9
34	IA94059-4	IABG2C0	299.7	1100.5	527.8	77.7	228.0	56.0	83.8	87.8
35	IA94056-7	IABG2C0	358.7	1231.6	561.1	66.9	208.3	63.2	85.1	99.3
36	IA94056-2	IABG2C0	385.6	1246.4	531.3	68.1	195.3	68.4	85.9	98.4
37	IA94049-5	IABG2C0	343.1	1131.4	545.3	64.6	196.4	67.3	84.5	97.5
38	IA94049-4	IABG2C0	402.1	1219.3	559.3	63.4	195.5	65.2	84.0	92.2
39	IA94031-7	IABG2C0	333.9	1085.4	559.6	72.0	204.7	59.8	83.6	95.7
40	IA94031-6	IABG2C0	367.4	1140.1	531.1	74.7	195.9	59.9	85.0	94.0
41	IA93150-5	IABG1C1	345.4	1119.6	530.0	69.0	213.2	60.2	88.6	96.6
42	IA93150-1	IABG1C1	312.2	1063.8	506.7	62.2	202.5	61.6	86.9	96.6
43	IA93108-5	IABG1C1	391.4	1720.2	486.7	66.8	226.4	60.4	89.8	102.8
44	IA93108-4	IABG1C1	318.4	1150.2	512.4	59.8	218.5	66.0	89.0	94.9
45	IA93089-4	IABG1C1	291.5	998.8	524.9	54.5	212.0	67.7	79.0	93.1
46	IA93089-1	IABG1C1	239.3	862.3	534.4	65.4	224.1	59.6	84.7	91.3
47	IA93067-5	IABG1C1	276.8	935.8	569.8	61.2	208.4	69.0	85.3	90.4
48	IA93067-2	IABG1C1	360.9	1152.4	564.7	53.3	198.7	70.9	82.4	94.0
49	IA93061-5	IABG1C1	389.5	1300.2	569.1	65.3	205.6	63.3	86.9	95.7
50	IA93061-3	IABG1C1	391.4	1296.1	533.1	64.7	199.8	68.2	84.9	94.9
51	IA93052-6	IABG1C1	259.4	1056.3	513.8	67.2	224.1	66.0	81.7	91.3
52	IA93052-5	IABG1C1	256.4	1031.8	495.3	70.3	225.5	66.7	86.0	94.9
53	IA93034-2	IABGPI	339.1	1084.4	462.2	59.2	211.2	77.8	87.0	87.8
54	IA93034-1	IABGPI	325.1	1075.9	491.6	56.2	202.6	76.4	84.8	83.4
55	IA93029-6	IABGPI	88.5	92.2
56	IA93029-4	IABGPI	227.7	1039.4	487.8	61.7	223.8	64.8	87.6	94.9

Table 5. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set five evaluated in 1996 at

Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
57	IA93028-3	IABG1C1	359.4	1161.1	531.1	71.0	186.7	68.5	86.7	93.1
58	IA93028-2	IABG1C1	354.9	1250.6	536.4	67.4	187.4	71.7	84.6	97.5
59	IA93014-3	IABGPI	337.2	1243.4	524.7	59.5	198.6	71.2	88.4	97.5
60	IA93014-1	IABGPI	370.4	1343.6	539.1	57.5	206.4	71.1	86.5	107.2
61	IA91509-4	IABG1C0	323.9	1042.5	544.4	60.7	187.0	67.7	87.3	92.2
62	IA91509-2	IABG1C0	382.7	1202.7	549.8	67.1	182.6	61.5	87.6	93.1
63	IA91504-2	IABG1C0	245.7	1016.7	564.7	49.6	199.8	74.1	87.3	98.4
64	IA91504-11	IABG1C0	263.1	1285.5	596.4	51.4	216.7	70.5	85.1	100.2
65	IA91500-8	IABG1C0	285.6	1174.6	556.0	65.3	218.2	63.5	88.1	100.2
66	IA91500-6	IABG1C0	266.3	1096.9	605.6	60.8	211.7	66.7	86.4	93.1
67	IA91486-2	IABG1C0	380.9	1246.2	537.6	62.8	207.4	66.7	85.9	95.7
68	IA91486-11	IABG1C0	339.0	1166.4	532.2	74.2	219.6	66.9	86.0	92.2
69	IA91485-4	IABG1C0	366.9	1333.1	555.3	62.9	214.8	54.2	88.6	98.4
70	IA91485-18	IABG1C0	315.3	1031.5	559.8	64.1	200.1	65.1	86.9	95.7
71	IA91479-6	IABG1C0	381.8	1231.9	542.9	65.2	199.6	72.4	86.5	97.5
72	IA91479-2	IABG1C0	361.9	1261.9	517.1	66.0	212.0	61.5	86.3	94.0
73	IA91478-6	IABG1C0	337.0	1090.7	541.1	64.5	183.9	70.2	82.0	87.8
74	IA91478-1	IABG1C0	329.4	1133.2	544.0	60.1	209.9	63.9	85.2	92.2
75	IA91470-3	IABG1C0	379.5	1308.3	522.0	56.9	218.0	63.0	87.2	99.3
76	IA91470-10	IABG1C0	263.0	1179.7	469.8	59.2	229.4	68.6	86.4	95.7
77	IA91462-17	IABG1C0	92.7	100.2
78	IA91462-11	IABG1C0	395.4	1179.7	571.3	57.0	175.5	66.1	83.0	96.6
79	IA91448-3	IABG1C0	315.4	1139.1	562.2	59.2	192.7	72.6	86.3	100.2
80	IA91448-1	IABG1C0	309.9	1104.4	514.4	68.5	194.3	70.5	84.3	97.5
81	H688-11	Par. line	358.0	1296.7	519.6	61.0	191.7	69.7	85.2	95.7
82	IL85-6183-1	Par. line	346.7	1186.0	543.6	70.2	207.5	62.5	87.2	86.9
83	D921-255	Par. line	304.9	996.7	515.8	59.5	184.4	74.9	84.2	95.7
84	NO10-1	Par. line	258.3	1194.6	617.6	61.3	219.1	66.6	89.4	108.1

Table 5. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set five evaluated in 1996 at

Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	NO11-1	Par. line	87.8	112.6
86	Hazel	Check	327.3	1030.7	527.1	54.2	195.6	78.1	84.8	92.2
87	Hazel	Check	260.7	1029.4	516.0	63.3	210.0	75.2	86.5	88.7
88	Starter	Check	377.0	1206.8	553.1	65.9	191.0	67.0	84.2	92.2
89	Starter	Check	293.8	1001.2	510.9	60.5	197.2	66.1	85.8	87.8
90	Premier	Check	392.4	1339.2	569.1	73.5	194.9	62.9	87.5	96.6
91	Premier	Check	392.4	1335.4	557.8	68.9	186.3	65.9	87.0	96.6
92	Marion	Check	337.6	1246.9	579.6	67.8	178.9	77.8	87.0	105.5
93	Marion	Check	337.5	1168.0	547.3	71.7	175.8	77.1	87.3	104.6
94	Noble	Check	297.2	1063.9	534.0	53.3	197.7	63.2	85.5	94.0
95	Noble	Check	320.8	1132.1	540.7	51.8	206.6	62.2	86.0	94.0
96	Ogle	Check	311.2	1211.5	506.4	63.0	210.4	58.3	88.2	94.9
97	Ogle	Check	345.5	1341.7	543.8	53.6	207.0	59.3	86.7	95.7
98	Don	Check	360.7	1114.1	540.9	51.7	169.2	73.9	81.7	86.9
99	Don	Check	358.3	1127.3	523.8	52.8	175.2	75.4	82.8	88.7
100	IAN979-5-2	Check	338.3	1288.9	501.1	70.3	204.1	76.0	88.4	91.3
Mean [†]			310.8	1118.0	495.9	57.0	193.0	67.5	86.7	93.5
LSD [‡]	Entry vs Entry		164.1	397.1	63.0	9.6	12.1	3.5	3.9	7.3

[†] Mean of all entries evaluated in 1996 at Ames.

[‡] Least significant difference at the 0.05 probability level.

Table 6. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set one evaluated in 1996 at

Nashua, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
1	IA95196-7	IABG2C1	317.2	881.5	541.6	69.4	183.3	71.4	.	.
2	IA95196-5	IABG2C1	395.1	1103.1	508.0	65.2	184.6	78.9	.	.
3	IA95189-9	IABG2C1	219.1	640.4	.	74.1	227.6	62.1	.	.
4	IA95189-2	IABG2C1	253.7	793.7	436.7	66.6	229.0	61.1	.	.
5	IA95181-6	IABG2C1	297.0	560.9	479.3	79.8	224.5	60.3	.	.
6	IA95181-4	IABG2C1	262.4	789.4	446.0	68.8	217.1	66.1	.	.
7	IA95172-4	IABG2C1
8	IA95172-1	IABG2C1	334.5	911.1	515.8	79.0	199.0	77.5	.	.
9	IA95148-3	IABG2C1	276.8	785.2	505.8	81.2	198.9	64.9	.	.
10	IA95148-1	IABG2C1
11	IA95109-3	IABG2C1	325.9	798.1	515.6	74.7	205.9	69.6	.	.
12	IA95109-2	IABG2C1	314.3	763.6	506.2	75.7	207.8	62.1	.	.
13	IA95103-6	IABG2C1	299.9	933.2	485.1	72.4	215.2	62.3	.	.
14	IA95103-3	IABG2C1	317.2	951.5	519.6	70.5	208.2	69.9	.	.
15	IA95038-9	IABG2C1	392.2	1011.3	545.1	72.8	190.3	61.7	.	.
16	IA95038-7	IABG2C1	325.9	922.0	545.6	76.8	194.5	68.4	.	.
17	IA95032-9	IABG2C1	265.2	758.3	505.6	74.5	195.9	71.8	.	.
18	IA95032-6	IABG2C1	302.8	844.2	513.6	69.2	190.5	72.6	.	.
19	IA95029-4	IABG2C1	233.5	605.1	435.6	71.2	193.2	75.0	.	.
20	IA95029-3	IABG2C1	271.0	739.0	559.3	79.6	193.2	73.8	.	.
21	IA94192-7	IABG2C0	412.4	1277.0	552.9	75.8	213.6	68.9	.	.
22	IA94192-1	IABG2C0	297.0	1132.0	516.4	64.0	210.7	80.1	.	.
23	IA94190-10	IABG2C0	331.0	987.0	524.4	80.8	189.2	68.5	.	.
24	IA94190-1	IABG2C0	377.8	1039.4	530.0	73.9	192.8	71.2	.	.
25	IA94187-5	IABG2C0	291.2	841.8	484.9	63.4	199.9	67.2	.	.
26	IA94187-10	IABG2C0	377.8	1059.2	565.6	71.1	201.4	70.5	.	.
27	IA94178-6	IABG2C0	363.4	1063.2	549.6	70.0	183.1	75.5	.	.
28	IA94178-1	IABG2C0	285.4	1081.6	520.9	68.6	185.9	68.9	.	.

Table 6. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set one evaluated in 1996 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
29	IA94163-6	IABG2C0	302.8	994.7	474.9	66.6	214.1	60.5	.	.
30	IA94163-3	IABG2C0	276.8	908.4	480.2	66.0	203.7	62.6	.	.
31	IA94143-7	IABG2C0	363.4	994.4	497.3	72.6	188.9	80.6	.	.
32	IA94143-4	IABG2C0	337.4	1036.9	505.8	73.2	193.6	79.1	.	.
33	IA94059-6	IABG2C0	282.6	761.5	527.1	67.1	209.4	73.9	.	.
34	IA94059-4	IABG2C0	288.3	869.2	514.7	74.8	216.6	70.6	.	.
35	IA94056-7	IABG2C0	337.4	1079.1	528.0	72.6	199.5	65.4	.	.
36	IA94056-2	IABG2C0	285.4	958.6	481.8	70.0	219.3	66.0	.	.
37	IA94049-5	IABG2C0	403.8	1207.7	475.3	65.9	201.1	69.2	.	.
38	IA94049-4	IABG2C0	374.9	1137.9	476.7	66.9	198.8	68.5	.	.
39	IA94031-7	IABG2C0	.	.	540.4
40	IA94031-6	IABG2C0	308.5	878.0	561.6	77.6	202.2	63.2	.	.
41	IA93150-5	IABGPI	415.3	1139.6	531.6	65.6	192.2	70.9	.	.
42	IA93150-1	IABGPI	360.5	961.2	528.7	66.7	201.8	66.7	.	.
43	IA93108-5	IABG1C1	314.3	1073.0	511.8	66.7	187.1	65.5	.	.
44	IA93108-4	IABG1C1
45	IA93089-4	IABG1C1	429.7	1246.0	572.9	63.9	177.0	65.8	.	.
46	IA93089-1	IABG1C1	383.6	874.9	551.1	62.9	184.0	67.9	.	.
47	IA93067-5	IABGPI	363.4	1110.3	481.8	57.9	194.1	78.3	.	.
48	IA93067-2	IABGPI	351.8	967.8	514.7	65.4	192.8	77.3	.	.
49	IA93061-5	IABGPI	323.0	872.4	516.7	69.0	214.0	63.7	.	.
50	IA93061-3	IABGPI	276.8	815.2	510.4	58.9	213.1	70.0	.	.
51	IA93052-6	IABG1C1	268.1	945.5	450.0	62.7	219.8	67.6	.	.
52	IA93052-5	IABG1C1
53	IA93034-2	IABGPI	346.1	948.2	502.4	71.4	198.5	78.1	.	.
54	IA93034-1	IABGPI
55	IA93029-6	IABG1C1	386.5	1125.0	554.0	71.8	177.0	64.0	.	.
56	IA93029-4	IABG1C1	337.4	977.8	505.1	72.3	180.1	73.8	.	.

Table 6. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set one evaluated in 1996 at

Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
57	IA93028-3	IABGPI	392.2	1044.5	514.4	54.2	195.6	76.1	.	.
58	IA93028-2	IABGPI	305.7	900.6	495.6	50.3	211.8	68.2	.	.
59	IA93014-3	IABGPI	380.7	1033.4	532.0	63.6	188.9	72.7	.	.
60	IA93014-1	IABGPI	357.6	1024.1	473.6	61.0	189.7	78.7	.	.
61	IA91509-4	IABGIC0	372.0	999.0	490.7	64.2	183.2	68.0	.	.
62	IA91509-2	IABGIC0	363.4	1243.7	500.7	59.8	197.4	67.3	.	.
63	IA91504-2	IABGIC0	311.4	1010.7	535.8	58.0	177.3	81.4	.	.
64	IA91504-11	IABGIC0	334.5	1000.8	544.4	58.6	188.4	74.9	.	.
65	IA91500-8	IABGIC0	386.5	1268.6	510.7	60.8	183.8	67.9	.	.
66	IA91500-6	IABGIC0	331.6	1025.9	461.3	57.0	166.2	78.5	.	.
67	IA91486-2	IABGIC0	305.7	947.1	533.8	62.6	191.3	60.4	.	.
68	IA91486-11	IABGIC0	305.7	946.4	542.4	58.3	188.3	64.2	.	.
69	IA91485-4	IABGIC0	426.9	1193.1	562.9	66.9	160.9	67.4	.	.
70	IA91485-18	IABGIC0	247.9	675.3	519.8	68.5	179.9	61.7	.	.
71	IA91479-6	IABGIC0	294.1	941.1	551.1	57.8	178.5	70.3	.	.
72	IA91479-2	IABGIC0	308.5	1103.7	545.3	56.0	196.3	68.4	.	.
73	IA91478-6	IABGIC0	374.9	1114.4	553.6	61.0	188.7	64.3	.	.
74	IA91478-1	IABGIC0	374.9	1064.8	550.4	56.0	176.9	68.5	.	.
75	IA91470-3	IABGIC0	386.5	1258.8	567.8	64.4	205.9	70.1	.	.
76	IA91470-10	IABGIC0	429.7	1197.5	524.4	69.6	190.4	64.0	.	.
77	IA91462-17	IABGIC0	377.8	1213.0	553.8	57.4	188.2	75.5	.	.
78	IA91462-11	IABGIC0	302.8	906.7	554.7	60.6	192.7	72.0	.	.
79	IA91448-3	IABGIC0	400.9	1336.5	496.9	59.4	200.9	70.4	.	.
80	IA91448-1	IABGIC0	374.9	1216.1	547.3	60.1	200.5	69.7	.	.
81	IL82-2154	Par. line	288.3	1003.8	476.2	62.6	213.5	61.0	.	.
82	D831-1-571	Par. line	328.7	924.6	546.9	65.1	201.1	70.9	.	.
83	OA926-2	Par. line	424.0	1245.0	542.7	61.0	175.6	66.8	.	.
84	PI412928	Par. line	328.7	1026.4	480.2	68.3	224.1	58.2	.	.

Table 6. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set one evaluated in 1996 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	PI504593	Par. line	297.0	867.5	522.7	59.7	190.4	72.2	.	.
86	Hazel	Check	435.5	1174.3	533.3	56.6	194.1	82.0	.	.
87	Hazel	Check	392.2	1127.3	531.1	56.8	195.7	80.4	.	.
88	Starter	Check	340.3	861.3	543.1	60.0	187.9	69.7	.	.
89	Starter	Check	348.9	987.6	556.7	59.5	183.7	70.9	.	.
90	Premier	Check	475.9	1027.4	529.3	68.3	182.8	68.6	.	.
91	Premier	Check	358.3	1045.6	554.0	71.3	186.6	66.0	.	.
92	Marion	Check	458.6	1332.2	535.8	66.8	176.6	77.0	.	.
93	Marion	Check	421.1	1177.3	549.1	69.3	179.0	73.9	.	.
94	Noble	Check	380.7	1125.2	536.7	59.9	207.0	62.9	.	.
95	Noble	Check	357.6	1023.7	566.4	62.0	192.8	62.3	.	.
96	Ogle	Check	299.9	1184.7	488.7	59.1	191.9	65.1	.	.
97	Ogle	Check	383.6	1212.4	509.8	55.9	178.1	74.8	.	.
98	Don	Check	409.5	1056.1	507.3	51.1	168.3	77.7	.	.
99	Don	Check	366.3	857.7	508.0	70.7	203.6	76.1	.	.
100	IAN979-5-2	Check	328.7	1001.4	488.0	71.3	191.8	78.4	.	.
Mean [†]			339.5	1020.6	533.2	60.7	181.6	69.3		
LSD [‡]	Entry vs Entry		153.3	534.5	47.1	9.8	20.5	6.8		

[†] Mean of all entries evaluated in 1996 at Nashua.

[‡] Least significant difference at the 0.05 probability level.

Table 7. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set two evaluated in 1996 at Nashua, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
1	IA95196-7	IABG2C1	238.3	.	476.9	81.2	191.3	68.6	.	.
2	IA95196-5	IABG2C1	242.6	.	508.7	73.7	204.9	72.1	.	.
3	IA95189-9	IABG2C1
4	IA95189-2	IABG2C1
5	IA95181-6	IABG2C1
6	IA95181-4	IABG2C1
7	IA95172-4	IABG2C1	246.9	.	470.9	79.5	195.8	57.3	.	.
8	IA95172-1	IABG2C1
9	IA95148-3	IABG2C1	325.0	.	518.9	71.1	194.6	83.7	.	.
10	IA95148-1	IABG2C1	216.6	.	516.2	70.3	196.3	81.4	.	.
11	IA95109-3	IABG2C1	346.6	.	497.6	68.6	179.6	66.5	.	.
12	IA95109-2	IABG2C1	220.9	.	457.1	69.8	179.8	69.5	.	.
13	IA95103-6	IABG2C1	160.2	.	370.4	62.5	204.6	72.3	.	.
14	IA95103-3	IABG2C1	372.7	.	535.8	65.2	202.4	58.5	.	.
15	IA95038-9	IABG2C1	281.6	.	506.4	68.7	199.6	65.4	.	.
16	IA95038-7	IABG2C1	294.6	.	527.3	73.5	206.5	61.2	.	.
17	IA95032-9	IABG2C1	281.6	.	495.1	68.8	195.9	63.1	.	.
18	IA95032-6	IABG2C1	225.2	.	472.7	75.0	203.6	67.8	.	.
19	IA95029-4	IABG2C1	364.0	.	545.3	72.1	176.9	73.9	.	.
20	IA95029-3	IABG2C1	411.7	.	541.8	71.2	175.4	69.7	.	.
21	IA94192-7	IABG2C0	372.7	.	559.8	67.8	186.3	75.4	.	.
22	IA94192-1	IABG2C0	437.7	.	490.2	64.5	198.8	71.0	.	.
23	IA94190-10	IABG2C0	398.7	.	530.2	74.7	203.9	58.9	.	.
24	IA94190-1	IABG2C0	403.0	.	550.7	73.1	198.9	64.5	.	.
25	IA94187-5	IABG2C0	411.7	.	526.7	64.3	179.4	82.1	.	.
26	IA94187-10	IABG2C0	368.3	.	530.0	59.2	190.3	80.1	.	.
27	IA94178-6	IABG2C0	264.3	.	542.9	70.2	212.2	53.9	.	.
28	IA94178-1	IABG2C0	272.9	.	529.1	73.9	218.1	46.5	.	.

Table 7. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set two evaluated in 1996 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
29	IA94163-6	IABG2C0	325.0	.	552.7	68.1	203.5	72.0	.	.
30	IA94163-3	IABG2C0	420.3	.	541.3	61.5	171.8	82.3	.	.
31	IA94143-7	IABG2C0	212.2	.	434.2	77.1	227.7	60.8	.	.
32	IA94143-4	IABG2C0	281.6	.	450.0	83.1	202.3	64.5	.	.
33	IA94059-6	IABG2C0	377.0	.	508.7	71.9	200.2	72.7	.	.
34	IA94059-4	IABG2C0	351.0	.	560.4	67.8	167.4	71.7	.	.
35	IA94056-7	IABG2C0	268.6	.	481.1	65.0	220.9	57.9	.	.
36	IA94056-2	IABG2C0	259.9	.	470.4	66.8	227.6	59.8	.	.
37	IA94049-5	IABG2C0	381.3	.	527.8	65.0	182.5	72.1	.	.
38	IA94049-4	IABG2C0	355.3	.	578.9	72.5	189.1	60.3	.	.
39	IA94031-7	IABG2C0	229.6	.	502.4	77.0	208.8	64.8	.	.
40	IA94031-6	IABG2C0	212.2	.	466.2	69.8	229.1	63.2	.	.
41	IA93150-5	IABG1C1	468.0	.	557.8	71.6	202.3	62.2	.	.
42	IA93150-1	IABG1C1	411.7	.	581.8	71.3	202.4	63.3	.	.
43	IA93108-5	IABG1C1	407.3	.	544.7	66.1	208.9	61.8	.	.
44	IA93108-4	IABG1C1	299.0	.	513.3	67.9	217.9	57.9	.	.
45	IA93089-4	IABG1C1	498.4	.	533.8	62.6	179.6	72.1	.	.
46	IA93089-1	IABG1C1	372.7	.	546.0	70.5	174.6	64.4	.	.
47	IA93067-5	IABG1C1	390.0	.	510.2	68.9	198.9	69.3	.	.
48	IA93067-2	IABG1C1	437.7	.	518.4	72.3	207.2	69.9	.	.
49	IA93061-5	IABG1C1	429.0	.	520.4	65.6	179.7	63.9	.	.
50	IA93061-3	IABG1C1	325.0	.	492.7	59.8	189.5	66.1	.	.
51	IA93052-6	IABG1C1	368.3	.	510.4	63.4	190.4	77.8	.	.
52	IA93052-5	IABG1C1	390.0	.	526.9	68.5	196.3	74.2	.	.
53	IA93034-2	IABG1C1	450.7	.	514.0	61.8	192.8	77.4	.	.
54	IA93034-1	IABG1C1	372.7	.	529.6	63.7	199.6	70.1	.	.
55	IA93029-6	IABG1C1	251.3	.	498.7	66.6	209.6	60.5	.	.
56	IA93029-4	IABG1C1	190.6	.	456.7	69.4	214.4	62.2	.	.

Table 7. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set two evaluated in 1996 at

Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
57	IA93028-3	IABGIC1	463.7	.	543.3	59.1	184.8	69.9	.	.
58	IA93028-2	IABGIC1	485.4	.	489.3	60.2	176.7	71.0	.	.
59	IA93014-3	IABGIC1	485.4	.	547.6	57.8	175.7	75.1	.	.
60	IA93014-1	IABGIC1	450.7	.	511.6	56.5	180.1	70.7	.	.
61	IA91509-4	IABGIC0	303.3	.	468.4	55.5	182.7	70.8	.	.
62	IA91509-2	IABGIC0	403.0	.	508.2	64.5	170.2	66.5	.	.
63	IA91504-2	IABGIC0	251.3	.	503.8	60.2	177.5	67.7	.	.
64	IA91504-11	IABGIC0
65	IA91500-8	IABGIC0	372.7	.	470.7	51.7	178.8	86.2	.	.
66	IA91500-6	IABGIC0	351.0	.	489.6	55.9	190.1	80.2	.	.
67	IA91486-2	IABGIC0
68	IA91486-11	IABGIC0
69	IA91485-4	IABGIC0	294.6	.	465.8	61.5	200.6	64.3	.	.
70	IA91485-18	IABGIC0	320.6	.	556.0	68.8	196.6	61.5	.	.
71	IA91479-6	IABGIC0	355.3	.	528.9	57.3	177.6	68.4	.	.
72	IA91479-2	IABGIC0	264.3	.	479.1	58.7	156.2	70.2	.	.
73	IA91478-6	IABGIC0	468.0	.	537.3	56.7	187.4	76.9	.	.
74	IA91478-1	IABGIC0	489.7	.	543.6	67.6	176.2	74.2	.	.
75	IA91470-3	IABGIC0	411.7	.	540.4	60.9	185.7	75.9	.	.
76	IA91470-10	IABGIC0	299.0	.	464.0	66.4	194.4	64.1	.	.
77	IA91462-17	IABGIC0	390.0	.	499.3	59.5	201.3	66.6	.	.
78	IA91462-11	IABGIC0	411.7	.	540.2	60.5	191.9	66.7	.	.
79	IA91448-3	IABGIC0	272.9	.	471.8	61.5	192.8	65.1	.	.
80	IA91448-1	IABGIC0	394.3	.	546.2	59.8	192.6	73.6	.	.
81	H52-5	Par. line	381.3	.	540.2	56.1	181.3	46.8	.	.
82	P7869D1-5†	Par. line	359.7	.	519.8	61.6	209.5	61.9	.	.
83	NO5-1	Par. line	233.9	.	625.8	53.8	187.6	60.8	.	.
84	CO5406...380	Par. line

Table 7. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set two evaluated in 1996 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	PI504601	Par. line	390.0	.	560.7	53.7	199.6	74.3	.	.
86	Hazel	Check	450.7	.	563.6	58.4	181.7	82.2	.	.
87	Hazel	Check	446.4	.	537.3	63.5	193.0	78.7	.	.
88	Starter	Check	403.0	.	549.6	64.5	182.4	71.7	.	.
89	Starter	Check	364.0	.	563.8	61.7	178.1	70.8	.	.
90	Premier	Check	359.7	.	512.0	69.6	183.7	64.4	.	.
91	Premier	Check	385.7	.	590.4	71.3	182.9	66.2	.	.
92	Marion	Check	515.7	.	521.3	72.1	177.3	75.7	.	.
93	Marion	Check	390.0	.	493.1	69.5	166.6	77.2	.	.
94	Noble	Check	377.0	.	521.6	52.9	189.7	66.2	.	.
95	Noble	Check	442.0	.	537.1	55.2	195.7	63.1	.	.
96	Ogle	Check	429.0	.	510.2	54.2	190.5	62.2	.	.
97	Ogle	Check	424.7	.	520.4	58.2	188.6	64.6	.	.
98	Don	Check	372.7	.	502.4	52.3	161.9	78.9	.	.
99	Don	Check	346.6	.	500.7	54.3	171.1	74.8	.	.
100	IAN979-5-2	Check	351.0	.	498.2	72.3	196.7	78.9	.	.
Mean [†]			339.5		533.2	60.7	181.6	69.3		
LSD [‡]	Entry vs Entry		153.3		47.1	9.8	20.5	6.8		

[†] Mean of all entries evaluated in 1996 at Nashua.

[‡] Least significant difference at the 0.05 probability level.

Table 8. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set three evaluated in 1996 at Nashua, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
1	IA95196-7	IABG2C1
2	IA95196-5	IABG2C1	187.3	649.2	517.8	81.2	184.5	68.9	.	.
3	IA95189-9	IABG2C1	378.7	1017.0	500.4	71.5	202.8	79.5	.	.
4	IA95189-2	IABG2C1	314.9	898.6	547.3	78.9	199.0	69.5	.	.
5	IA95181-6	IABG2C1	344.6	1034.0	505.1	69.6	205.5	72.0	.	.
6	IA95181-4	IABG2C1	297.9	835.2	546.2	70.2	213.5	68.9	.	.
7	IA95172-4	IABG2C1	217.1	746.4	511.1	77.8	205.4	60.3	.	.
8	IA95172-1	IABG2C1	225.6	742.2	518.4	75.5	198.8	63.8	.	.
9	IA95148-3	IABG2C1	208.6	767.6	514.9	71.6	203.5	66.1	.	.
10	IA95148-1	IABG2C1	357.4	979.0	534.9	76.3	193.2	65.8	.	.
11	IA95109-3	IABG2C1	204.3	712.6	485.3	69.8	201.1	72.6	.	.
12	IA95109-2	IABG2C1	183.1	670.3	498.0	80.2	210.8	66.0	.	.
13	IA95103-6	IABG2C1	208.6	780.3	463.1	72.0	211.6	57.2	.	.
14	IA95103-3	IABG2C1	225.6	809.9	514.4	75.2	209.4	61.7	.	.
15	IA95038-9	IABG2C1	255.4	898.6	484.9	74.7	195.6	65.4	.	.
16	IA95038-7	IABG2C1	183.1	683.0	467.6	80.1	193.7	64.6	.	.
17	IA95032-9	IABG2C1	166.1	678.8	361.8	65.9	195.1	59.8	.	.
18	IA95032-6	IABG2C1	285.1	953.6	475.6	69.3	210.6	59.5	.	.
19	IA95029-4	IABG2C1	242.6	932.5	438.4	83.3	212.2	60.2	.	.
20	IA95029-3	IABG2C1
21	IA94192-7	IABG2C0	302.1	886.0	495.3	69.7	199.4	71.1	.	.
22	IA94192-1	IABG2C0	336.1	957.8	544.7	69.3	202.7	69.0	.	.
23	IA94190-10	IABG2C0	323.4	962.1	497.8	75.3	191.9	61.4	.	.
24	IA94190-1	IABG2C0	251.1	822.5	484.2	75.7	192.2	58.2	.	.
25	IA94187-5	IABG2C0	382.9	1084.7	558.4	72.0	197.3	74.4	.	.
26	IA94187-10	IABG2C0	357.4	1021.3	578.0	69.6	194.5	73.2	.	.
27	IA94178-6	IABG2C0	276.6	835.2	516.2	76.9	206.3	56.8	.	.
28	IA94178-1	IABG2C0	285.1	894.4	497.1	78.0	203.9	55.0	.	.

Table 8. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set three evaluated in 1996 at

Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
29	IA94163-6	IABG2C0
30	IA94163-3	IABG2C0	289.4	962.1	509.8	88.2	215.6	54.5	.	.
31	IA94143-7	IABG2C0	229.8	894.4	506.7	68.7	212.2	56.5	.	.
32	IA94143-4	IABG2C0	289.4	970.5	486.4	66.9	218.2	58.2	.	.
33	IA94059-6	IABG2C0	217.1	750.7	470.0	66.0	209.9	66.7	.	.
34	IA94059-4	IABG2C0	259.6	881.7	500.4	60.7	211.0	63.7	.	.
35	IA94056-7	IABG2C0	310.6	898.6	511.1	76.8	193.6	64.3	.	.
36	IA94056-2	IABG2C0	404.2	1101.6	537.8	74.4	188.9	65.3	.	.
37	IA94049-5	IABG2C0	272.4	835.2	508.9	79.7	191.2	65.9	.	.
38	IA94049-4	IABG2C0	293.6	890.2	487.8	79.7	215.1	54.0	.	.
39	IA94031-7	IABG2C0	429.7	1088.9	533.8	63.6	181.5	68.1	.	.
40	IA94031-6	IABG2C0	340.4	856.4	543.3	78.1	183.6	71.4	.	.
41	IA93150-5	IABG1C1	459.4	1338.4	530.9	70.6	205.9	68.3	.	.
42	IA93150-1	IABG1C1	353.2	1131.2	548.7	74.3	206.7	68.8	.	.
43	IA93108-5	IABGPI	310.6	1025.5	486.0	58.5	205.6	70.9	.	.
44	IA93108-4	IABGPI	331.9	1008.6	456.7	65.3	210.2	75.2	.	.
45	IA93089-4	IABGPI	493.5	1236.9	487.8	65.4	179.5	76.4	.	.
46	IA93089-1	IABGPI	446.7	1203.1	508.9	67.3	175.2	71.9	.	.
47	IA93067-5	IABG1C1	399.9	1097.4	504.4	60.4	199.7	67.6	.	.
48	IA93067-2	IABG1C1	319.1	932.5	521.3	68.5	203.2	62.0	.	.
49	IA93061-5	IABG1C1	234.1	1021.3	472.2	58.4	200.6	74.7	.	.
50	IA93061-3	IABG1C1	365.9	1072.0	535.3	59.8	194.8	72.6	.	.
51	IA93052-6	IABG1C1	357.4	1012.8	502.4	73.2	188.8	69.4	.	.
52	IA93052-5	IABG1C1	344.6	1012.8	490.4	68.3	186.1	76.8	.	.
53	IA93034-2	IABG1C1	353.2	1055.1	527.3	74.9	194.8	76.1	.	.
54	IA93034-1	IABG1C1	340.4	970.5	552.2	75.0	198.9	75.2	.	.
55	IA93029-6	IABGPI	476.5	1355.3	491.1	70.6	184.7	74.8	.	.
56	IA93029-4	IABGPI	382.9	1135.4	475.8	59.1	175.9	74.3	.	.

Table 8. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set three evaluated in 1996 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
57	IA93028-3	IABGPI	374.4	1021.3	434.0	55.3	202.3	80.6	.	.
58	IA93028-2	IABGPI
59	IA93014-3	IABG1C1	450.9	1283.4	502.0	68.5	170.3	70.8	.	.
60	IA93014-1	IABG1C1	399.9	1076.2	531.1	72.0	163.1	73.6	.	.
61	IA91509-4	IABG1C0	378.7	847.9	532.4	62.3	182.5	76.7	.	.
62	IA91509-2	IABG1C0	331.9	979.0	542.2	62.0	194.8	81.5	.	.
63	IA91504-2	IABG1C0	225.6	805.6	502.2	63.4	197.7	70.9	.	.
64	IA91504-11	IABG1C0	374.4	1173.5	487.3	55.2	167.9	66.3	.	.
65	IA91500-8	IABG1C0	382.9	1034.0	559.8	61.2	186.5	70.2	.	.
66	IA91500-6	IABG1C0	336.1	1211.5	511.3	63.4	191.3	66.4	.	.
67	IA91486-2	IABG1C0	280.9	801.4	503.1	51.9	158.1	73.6	.	.
68	IA91486-11	IABG1C0	340.4	1046.6	567.3	52.1	208.3	73.2	.	.
69	IA91485-4	IABG1C0	229.8	759.1	500.7	68.7	176.0	79.2	.	.
70	IA91485-18	IABG1C0	361.7	1063.6	503.6	63.3	185.8	75.6	.	.
71	IA91479-6	IABG1C0	314.9	919.8	486.0	51.4	200.5	65.0	.	.
72	IA91479-2	IABG1C0	297.9	911.3	480.7	55.4	173.4	71.1	.	.
73	IA91478-6	IABG1C0	327.6	1177.7	485.1	62.9	186.4	75.1	.	.
74	IA91478-1	IABG1C0	404.2	1131.2	457.6	62.3	206.5	73.9	.	.
75	IA91470-3	IABG1C0	374.4	1080.5	491.3	63.2	187.8	72.2	.	.
76	IA91470-10	IABG1C0	416.9	1076.2	516.7	64.5	188.8	68.9	.	.
77	IA91462-17	IABG1C0	255.4	1055.1	485.6	65.9	221.8	73.1	.	.
78	IA91462-11	IABG1C0	374.4	991.7	520.4	65.7	193.9	77.2	.	.
79	IA91448-3	IABG1C0	408.4	1131.2	562.4	65.5	186.3	59.0	.	.
80	IA91448-1	IABG1C0	378.7	1114.3	504.2	62.1	168.2	68.2	.	.
81	H87-7-4	Par. line	268.1	1025.5	531.6	57.7	194.8	69.3	.	.
82	MO07929	Par. line	378.7	1105.8	493.1	54.8	193.6	82.5	.	.
83	MN88156	Par. line	276.6	898.6	506.2	68.6	209.6	56.9	.	.
84	NO4-8	Par. line	293.6	966.3	600.4	53.2	181.3	72.7	.	.

Table 8. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set three evaluated in 1996 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	PI361884	Par. line	361.7	1008.6	462.4	62.4	168.4	72.5	.	.
86	Hazel	Check	412.7	1084.7	522.0	56.5	185.8	81.8	.	.
87	Hazel	Check	425.4	1127.0	522.2	58.8	189.0	83.1	.	.
88	Starter	Check	340.4	936.7	543.3	62.3	184.0	71.5	.	.
89	Starter	Check	340.4	957.8	557.4	58.1	181.1	72.3	.	.
90	Premier	Check	259.6	835.2	579.8	63.4	168.9	68.9	.	.
91	Premier	Check	357.4	991.7	592.9	70.0	177.4	66.4	.	.
92	Marion	Check	472.2	1338.4	551.2	67.0	161.7	77.5	.	.
93	Marion	Check	485.0	1241.1	530.8	67.8	172.4	77.4	.	.
94	Noble	Check	425.4	1211.5	551.8	53.8	200.1	63.1	.	.
95	Noble	Check	391.4	1186.2	570.9	48.6	199.1	64.1	.	.
96	Ogle	Check	353.2	1101.6	465.0	53.7	191.6	63.9	.	.
97	Ogle	Check	310.6	1034.0	492.6	54.2	192.0	65.3	.	.
98	Don	Check	344.6	907.1	545.2	55.8	164.3	78.9	.	.
99	Don	Check	289.4	788.7	536.9	53.3	161.2	77.7	.	.
100	IAN979-5-2	Check	297.9	919.8	497.8	65.9	179.9	81.8	.	.
Mean†			339.5	1020.6	533.2	60.7	181.6	69.3		
LSD‡	Entry vs Entry		153.3	534.5	47.1	9.8	20.5	6.8		

† Mean of all entries evaluated in 1996 at Nashua.

‡ Least significant difference at the 0.05 probability level.

Table 9. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set four evaluated in 1996 at Nashua, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
1	IA95196-7	IABG2C1
2	IA95196-5	IABG2C1	215.5	747.8	508.1	.	190.4	50.9	.	.
3	IA95189-9	IABG2C1
4	IA95189-2	IABG2C1	242.8	823.2	458.0
5	IA95181-6	IABG2C1	235.0	767.6	465.4	.	187.4	55.0	.	.
6	IA95181-4	IABG2C1	215.5	771.6	510.4	.	199.7	51.0	.	.
7	IA95172-4	IABG2C1
8	IA95172-1	IABG2C1	289.5	1081.1	469.1	.	193.4	58.6	.	.
9	IA95148-3	IABG2C1	402.4	1085.1	500.8	.	181.4	54.1	.	.
10	IA95148-1	IABG2C1	301.2	918.4	498.9	.	186.6	62.7	.	.
11	IA95109-3	IABG2C1
12	IA95109-2	IABG2C1	203.8	747.8	462.3	.	199.2	56.3	.	.
13	IA95103-6	IABG2C1	246.7	835.1	518.0
14	IA95103-3	IABG2C1	305.1	1009.7	538.4	.	185.9	58.6	.	.
15	IA95038-9	IABG2C1	199.9	684.3	500.6	.	191.8	53.4	.	.
16	IA95038-7	IABG2C1	199.9	720.0	422.4
17	IA95032-9	IABG2C1	242.8	759.7	453.9	.	191.2	53.0	.	.
18	IA95032-6	IABG2C1	332.3	716.0	529.0	.	184.6	59.9	.	.
19	IA95029-4	IABG2C1	355.7	989.8	489.2	.	192.2	55.7	.	.
20	IA95029-3	IABG2C1	199.9	723.9	477.0	.	207.7	48.3	.	.
21	IA94192-7	IABG2C0	371.2	1009.7	554.1	.	178.7	56.8	.	.
22	IA94192-1	IABG2C0	406.3	1093.0	533.0	.	177.0	63.1	.	.
23	IA94190-10	IABG2C0	468.6	1235.9	525.0	.	185.8	52.3	.	.
24	IA94190-1	IABG2C0	316.7	977.9	512.8	.	195.4	47.2	.	.
25	IA94187-5	IABG2C0	402.4	1140.7	534.2	.	183.4	58.7	.	.
26	IA94187-10	IABG2C0	456.9	1224.0	531.6
27	IA94178-6	IABG2C0	480.3	1220.0	529.0	.	182.1	57.9	.	.
28	IA94178-1	IABG2C0	394.6	1120.8	528.7	.	177.9	64.3	.	.

Table 9. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set four evaluated in 1996 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
29	IA94163-6	IABG2C0	375.1	1045.4	541.2	.	168.2	62.2	.	.
30	IA94163-3	IABG2C0	375.1	1013.7	583.0	.	172.6	64.3	.	.
31	IA94143-7	IABG2C0	277.8	981.9	417.0	.	199.9	46.9	.	.
32	IA94143-4	IABG2C0
33	IA94059-6	IABG2C0	258.3	886.7	482.6	.	190.1	54.5	.	.
34	IA94059-4	IABG2C0	382.9	1124.8	512.4
35	IA94056-7	IABG2C0	250.6	819.2	465.7	.	191.0	52.9	.	.
36	IA94056-2	IABG2C0	258.3	906.5	438.7	.	193.8	49.7	.	.
37	IA94049-5	IABG2C0	262.2	1009.7	486.0	.	195.1	52.9	.	.
38	IA94049-4	IABG2C0	242.8	1045.4	544.4	.	194.5	53.0	.	.
39	IA94031-7	IABG2C0	254.5	878.7	540.3	.	183.5	48.5	.	.
40	IA94031-6	IABG2C0	332.3	1069.2	498.2	.	178.8	54.5	.	.
41	IA93150-5	IABGPI	382.9	1081.1	439.3
42	IA93150-1	IABGPI	320.6	1005.7	413.7	.	178.1	57.6	.	.
43	IA93108-5	IABG1C1	363.5	1160.5	498.1	.	187.8	56.4	.	.
44	IA93108-4	IABG1C1	406.3	1231.9	551.3	.	182.0	66.0	.	.
45	IA93089-4	IABG1C1
46	IA93089-1	IABG1C1	277.8	930.3	502.0	.	179.0	56.8	.	.
47	IA93067-5	IABGPI	382.9	1041.4	539.7	.	167.3	61.0	.	.
48	IA93067-2	IABGPI
49	IA93061-5	IABGPI	277.8	1013.7	434.4	.	172.0	60.0	.	.
50	IA93061-3	IABGPI	418.0	1156.5	514.2	.	168.2	63.3	.	.
51	IA93052-6	IABG1C1	410.2	1196.2	502.9	.	186.5	57.7	.	.
52	IA93052-5	IABG1C1	347.9	1200.2	526.2	.	185.5	54.8	.	.
53	IA93034-2	IABG1C1	390.7	1085.1	505.8	.	192.7	55.3	.	.
54	IA93034-1	IABG1C1	301.2	993.8	488.7	.	190.5	54.9	.	.
55	IA93029-6	IABG1C1	612.6	1593.1	528.6	.	173.5	57.0	.	.
56	IA93029-4	IABG1C1	445.2	1319.2	539.8	.	181.0	57.1	.	.

Table 9. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set four evaluated in 1996 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
57	IA93028-3	IABGPI
58	IA93028-2	IABGPI	235.0	839.0	443.1	.	190.9	51.4	.	.
59	IA93014-3	IABG1C1	347.9	1013.7	496.8	.	181.5	58.8	.	.
60	IA93014-1	IABG1C1	316.7	1017.6	489.1	.	182.7	51.4	.	.
61	IA91509-4	IABG1C0	347.9	1132.7	485.6	.	172.4	55.5	.	.
62	IA91509-2	IABG1C0	375.1	974.0	515.1	.	180.0	57.9	.	.
63	IA91504-2	IABG1C0	394.6	1180.3	470.1	.	170.8	56.0	.	.
64	IA91504-11	IABG1C0	390.7	1081.1	478.6	.	156.2	57.8	.	.
65	IA91500-8	IABG1C0	301.2	1033.5	498.6
66	IA91500-6	IABG1C0	320.6	1069.2	501.1
67	IA91486-2	IABG1C0	410.2	1216.1	549.4	.	162.6	56.6	.	.
68	IA91486-11	IABG1C0	386.8	1156.5	502.2	.	163.5	54.5	.	.
69	IA91485-4	IABG1C0	305.1	1017.6	484.1	.	166.6	50.4	.	.
70	IA91485-18	IABG1C0	316.7	1081.1	482.4
71	IA91479-6	IABG1C0	441.3	1311.3	526.2
72	IA91479-2	IABG1C0	453.0	1255.7	502.7	.	170.4	63.9	.	.
73	IA91478-6	IABG1C0	441.3	1188.3	535.4	.	176.1	58.6	.	.
74	IA91478-1	IABG1C0	371.2	1041.4	510.9	.	168.7	56.3	.	.
75	IA91470-3	IABG1C0	425.8	1168.4	541.0	.	171.8	54.2	.	.
76	IA91470-10	IABG1C0	456.9	1204.2	491.3	.	184.7	51.9	.	.
77	IA91462-17	IABG1C0	355.7	1029.5	521.8	.	180.9	53.3	.	.
78	IA91462-11	IABG1C0
79	IA91448-3	IABG1C0	402.4	1101.0	543.3	.	177.0	52.3	.	.
80	IA91448-1	IABG1C0	371.2	1144.6	488.6	.	165.9	59.7	.	.
81	H730-12	Par. line	277.8	874.8	463.0	.	190.0	53.7	.	.
82	MN86226	Par. line	266.1	977.9	497.4	.	191.3	53.3	.	.
83	NO20-1	Par. line	305.1	1029.5	594.6
84	PI361886	Par. line	309.0	1045.4	443.6	.	159.5	66.1	.	.

Table 9. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set four evaluated in 1996 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	PI502955	Par. line	289.5	886.7	462.7	.	175.5	61.5	.	.
86	Hazel	Check	332.3	1025.6	518.4	.	181.8	58.3	.	.
87	Hazel	Check	309.0	886.7	548.9	.	179.2	65.3	.	.
88	Starter	Check	371.2	1053.3	511.0	.	172.9	59.1	.	.
89	Starter	Check	336.2	918.4	545.6	.	179.5	55.2	.	.
90	Premier	Check	336.2	1041.4	526.8	.	176.4	54.1	.	.
91	Premier	Check	305.1	906.5	556.4	.	165.2	54.5	.	.
92	Marion	Check	390.7	1104.9	520.9	.	166.5	60.2	.	.
93	Marion	Check	507.5	1394.6	532.4	.	169.3	59.9	.	.
94	Noble	Check
95	Noble	Check	351.8	1033.5	541.6	.	182.3	53.9	.	.
96	Ogle	Check	406.3	1192.2	531.1	.	169.5	56.0	.	.
97	Ogle	Check	414.1	1243.8	498.9	.	175.2	54.0	.	.
98	Don	Check	375.1	985.9	526.9	.	180.7	54.6	.	.
99	Don	Check	379.0	966.0	517.4	.	158.3	62.8	.	.
100	IAN979-5-2	Check
Mean [†]			339.5	1020.6	533.2		181.6	69.3		
LSD [‡]	Entry vs Entry		153.3	534.5	47.1		20.5	6.8		

[†] Mean of all entries evaluated in 1996 at Nashua.

[‡] Least significant difference at the 0.05 probability level.

Table 10. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set five evaluated in 1996 at Nashua, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
1	IA95196-7	IABG2C1	262.1	769.3	520.1	77.4	190.3	78.5	.	.
2	IA95196-5	IABG2C1	275.8	800.5	537.0	73.4	191.8	73.7	.	.
3	IA95189-9	IABG2C1	338.1	1075.8	525.8	71.2	190.8	68.1	.	.
4	IA95189-2	IABG2C1	363.7	1065.8	509.0	76.3	184.9	45.3	.	.
5	IA95181-6	IABG2C1	286.4	902.5	561.6	71.5	207.5	71.1	.	.
6	IA95181-4	IABG2C1	246.1	870.5	535.8	70.9	205.3	67.4	.	.
7	IA95172-4	IABG2C1
8	IA95172-1	IABG2C1	246.3	830.3	504.2	84.6	207.7	61.5	.	.
9	IA95148-3	IABG2C1	305.3	837.7	488.3	68.6	184.0	76.5	.	.
10	IA95148-1	IABG2C1	271.0	861.0	507.3	69.9	183.1	68.6	.	.
11	IA95109-3	IABG2C1	233.8	752.7	456.2	68.0	194.2	70.6	.	.
12	IA95109-2	IABG2C1	236.9	786.7	512.2	70.5	199.7	71.8	.	.
13	IA95103-6	IABG2C1	192.1	743.2	461.9	82.8	207.2	62.8	.	.
14	IA95103-3	IABG2C1	161.4	666.1	380.6	78.2	218.5	65.4	.	.
15	IA95038-9	IABG2C1	284.9	937.8	525.0	68.1	206.6	74.7	.	.
16	IA95038-7	IABG2C1	271.6	871.1	542.7	72.7	195.5	78.8	.	.
17	IA95032-9	IABG2C1	319.4	934.3	529.6	79.2	181.4	71.8	.	.
18	IA95032-6	IABG2C1	299.7	880.7	537.2	72.4	181.3	76.7	.	.
19	IA95029-4	IABG2C1	198.2	707.0	474.4	72.9	199.6	60.0	.	.
20	IA95029-3	IABG2C1	207.5	689.7	475.6	72.3	205.7	62.1	.	.
21	IA94192-7	IABG2C0	422.5	1113.0	538.0	73.6	201.7	61.9	.	.
22	IA94192-1	IABG2C0	364.4	1019.7	540.1	76.5	191.2	71.3	.	.
23	IA94190-10	IABG2C0	341.5	1017.2	519.0	69.0	203.4	79.1	.	.
24	IA94190-1	IABG2C0	338.9	959.5	531.3	71.9	190.3	84.1	.	.
25	IA94187-5	IABG2C0	245.8	1033.5	426.0	77.0	200.6	60.5	.	.
26	IA94187-10	IABG2C0	267.2	1027.0	442.6	71.4	181.4	70.5	.	.
27	IA94178-6	IABG2C0	347.1	1059.9	535.7	75.7	211.0	64.2	.	.
28	IA94178-1	IABG2C0	300.6	973.7	520.9	72.0	208.2	64.8	.	.

Table 10. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set five evaluated in 1996 at

Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
29	IA94163-6	IABG2C0	323.9	995.7	566.8	74.3	190.8	71.2	.	.
30	IA94163-3	IABG2C0	249.2	802.8	543.8	71.5	200.8	78.1	.	.
31	IA94143-7	IABG2C0	318.8	999.5	517.0	65.0	197.5	68.4	.	.
32	IA94143-4	IABG2C0	345.1	925.2	562.8	61.0	193.5	72.1	.	.
33	IA94059-6	IABG2C0	332.1	941.8	496.8	72.0	198.6	64.1	.	.
34	IA94059-4	IABG2C0	350.9	936.0	565.7	74.3	204.1	60.2	.	.
35	IA94056-7	IABG2C0	408.1	956.5	533.0	63.9	202.2	66.6	.	.
36	IA94056-2	IABG2C0	376.6	1066.2	500.0	60.9	184.7	72.1	.	.
37	IA94049-5	IABG2C0	430.6	1133.5	526.6	61.9	191.9	69.0	.	.
38	IA94049-4	IABG2C0	382.2	1028.1	534.8	62.7	188.1	67.5	.	.
39	IA94031-7	IABG2C0	342.7	1088.7	563.3	69.8	179.4	63.5	.	.
40	IA94031-6	IABG2C0	363.6	1013.4	506.7	74.5	181.6	64.0	.	.
41	IA93150-5	IABG1C1	410.0	1251.8	515.2	64.0	193.9	65.7	.	.
42	IA93150-1	IABG1C1	401.7	1061.2	509.9	65.9	191.7	65.3	.	.
43	IA93108-5	IABG1C1	322.9	1127.3	472.0	68.7	200.0	65.9	.	.
44	IA93108-4	IABG1C1	363.0	1141.8	485.1	64.7	198.0	65.6	.	.
45	IA93089-4	IABG1C1	327.8	949.2	518.9	59.5	193.1	71.5	.	.
46	IA93089-1	IABG1C1	259.8	785.3	520.0	64.7	218.1	61.7	.	.
47	IA93067-5	IABG1C1	263.4	815.9	558.7	59.1	203.5	71.1	.	.
48	IA93067-2	IABG1C1	328.0	949.5	578.3	57.9	197.2	71.4	.	.
49	IA93061-5	IABG1C1	426.6	1119.4	555.8	65.5	198.1	65.0	.	.
50	IA93061-3	IABG1C1	346.3	1013.2	520.8	60.6	204.6	69.9	.	.
51	IA93052-6	IABG1C1	211.9	759.4	476.6	62.0	217.0	69.5	.	.
52	IA93052-5	IABG1C1	193.0	774.3	489.2	65.3	230.2	64.7	.	.
53	IA93034-2	IABGPI	316.3	905.7	446.3	51.3	189.9	82.2	.	.
54	IA93034-1	IABGPI	380.7	1108.9	437.3	54.8	193.9	78.6	.	.
55	IA93029-6	IABGPI
56	IA93029-4	IABGPI	292.6	930.7	489.8	62.2	198.7	65.7	.	.

Table 10. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set five evaluated in 1996 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
57	IA93028-3	IABG1C1	446.6	1137.5	533.8	65.7	174.4	74.0	.	.
58	IA93028-2	IABG1C1	478.9	1182.0	510.3	70.5	180.8	76.8	.	.
59	IA93014-3	IABGPI	355.0	1137.8	466.6	56.4	179.6	77.8	.	.
60	IA93014-1	IABGPI	390.8	1160.6	495.2	56.3	193.9	74.4	.	.
61	IA91509-4	IABG1C0	262.1	963.7	494.2	65.4	181.0	63.1	.	.
62	IA91509-2	IABG1C0	352.1	1024.8	504.7	67.8	179.2	68.8	.	.
63	IA91504-2	IABG1C0	372.0	1071.7	537.6	51.7	184.5	75.9	.	.
64	IA91504-11	IABG1C0	288.9	1084.4	497.8	50.9	199.3	72.5	.	.
65	IA91500-8	IABG1C0	279.8	1053.6	530.4	55.6	213.4	63.9	.	.
66	IA91500-6	IABG1C0	285.5	936.5	546.1	55.5	195.9	68.0	.	.
67	IA91486-2	IABG1C0	411.2	1148.7	487.6	61.6	194.0	69.3	.	.
68	IA91486-11	IABG1C0	453.4	1217.8	531.2	66.5	203.4	66.8	.	.
69	IA91485-4	IABG1C0	447.5	1224.1	497.0	54.2	201.7	58.8	.	.
70	IA91485-18	IABG1C0	415.2	1118.8	517.1	62.0	187.9	65.6	.	.
71	IA91479-6	IABG1C0	280.6	977.4	532.6	64.1	192.5	71.6	.	.
72	IA91479-2	IABG1C0	430.0	1211.9	513.1	59.6	185.4	67.5	.	.
73	IA91478-6	IABG1C0	326.4	929.5	517.2	62.2	204.6	68.4	.	.
74	IA91478-1	IABG1C0	322.5	970.9	557.6	56.3	202.8	68.5	.	.
75	IA91470-3	IABG1C0	380.4	1053.7	543.4	54.4	181.8	68.6	.	.
76	IA91470-10	IABG1C0	283.6	1073.3	463.1	55.9	218.4	69.9	.	.
77	IA91462-17	IABG1C0	334.3	1115.4	463.9	60.6	197.6	68.4	.	.
78	IA91462-11	IABG1C0	379.1	996.9	535.6	59.2	180.4	69.0	.	.
79	IA91448-3	IABG1C0	419.7	1166.1	559.3	62.5	174.2	75.1	.	.
80	IA91448-1	IABG1C0	475.1	1190.1	528.1	66.4	180.0	75.8	.	.
81	H688-11	Par. line	393.6	1150.4	521.9	62.0	185.9	75.6	.	.
82	IL85-6183-1	Par. line	312.9	1092.6	481.3	72.4	204.7	65.5	.	.
83	D921-255	Par. line	280.1	812.7	480.4	61.9	179.1	81.9	.	.
84	NO10-1	Par. line	302.3	1069.2	648.0	57.5	181.7	72.6	.	.

Table 10. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set five evaluated in 1996 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	NO11-1	Par. line	253.3	918.7	658.8	57.4	207.5	70.0	.	.
86	Hazel	Check	427.0	1108.0	537.4	55.3	180.2	85.8	.	.
87	Hazel	Check	359.6	1030.6	534.8	59.6	195.6	81.5	.	.
88	Starter	Check	318.6	929.4	545.1	64.1	187.9	71.3	.	.
89	Starter	Check	326.3	936.8	545.9	61.6	183.5	71.6	.	.
90	Premier	Check	397.1	1123.7	579.7	75.6	177.4	68.1	.	.
91	Premier	Check	358.8	1059.2	565.8	75.6	176.8	66.7	.	.
92	Marion	Check	433.0	1126.4	557.8	69.8	161.3	81.6	.	.
93	Marion	Check	472.6	1216.3	525.4	65.2	174.2	76.1	.	.
94	Noble	Check	310.6	1049.3	522.4	47.3	204.8	65.2	.	.
95	Noble	Check	370.6	1128.6	532.4	52.2	205.2	63.6	.	.
96	Ogle	Check	337.4	1172.9	501.1	58.1	194.2	62.3	.	.
97	Ogle	Check	383.8	1177.5	503.3	57.4	190.3	65.0	.	.
98	Don	Check	350.2	930.6	521.6	54.6	168.6	78.8	.	.
99	Don	Check	315.1	876.3	506.4	53.1	175.1	77.4	.	.
100	IAN979-5-2	Check	302.3	955.0	564.4	76.6	197.9	80.3	.	.
Mean [†]			339.5	1020.6	533.2	60.7	181.6	69.3		
LSD [‡]	Entry vs Entry		153.3	534.5	47.1	9.8	20.5	6.8		

[†] Mean of all entries evaluated in 1996 at Nashua.

[‡] Least significant difference at the 0.05 probability level.

Table 11. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set one evaluated in 1997 at

Ames, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β -Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
1	IA95196-7	IABG2C1	448.0	935.8	486.5	46.1	183.6	72.7	77.3	89.3
2	IA95196-5	IABG2C1	422.0	904.3	503.7	53.6	183.0	73.9	76.5	94.9
3	IA95189-9	IABG2C1	258.3	663.9	474.0	.	.	.	80.7	103.1
4	IA95189-2	IABG2C1	275.6	681.9	470.1	45.1	210.7	60.7	81.4	102.5
5	IA95181-6	IABG2C1	188.8	446.4	80.4	86.6
6	IA95181-4	IABG2C1	359.8	776.6	491.2	47.1	199.6	64.2	78.2	93.9
7	IA95172-4	IABG2C1	305.3	680.0	522.5	.	.	.	81.6	87.1
8	IA95172-1	IABG2C1	437.4	948.1	506.3	57.7	194.8	72.0	77.0	96.4
9	IA95148-3	IABG2C1	374.4	834.0	494.0	55.5	189.6	59.2	79.9	89.0
10	IA95148-1	IABG2C1	303.1	694.9	483.3	54.6	195.7	57.7	82.7	92.2
11	IA95109-3	IABG2C1	317.7	751.5	507.9	53.2	201.7	53.7	84.5	85.6
12	IA95109-2	IABG2C1	351.0	796.0	495.2	60.2	196.9	60.3	84.3	81.4
13	IA95103-6	IABG2C1	425.8	947.2	501.9	45.2	204.4	69.4	80.6	102.1
14	IA95103-3	IABG2C1	369.9	806.3	512.6	48.9	203.7	65.4	82.0	102.1
15	IA95038-9	IABG2C1	446.5	950.6	509.6	50.9	196.9	56.4	80.1	100.0
16	IA95038-7	IABG2C1	454.1	982.5	498.7	48.7	194.6	61.3	77.8	102.3
17	IA95032-9	IABG2C1	358.1	742.1	489.1	53.2	186.5	71.2	78.5	93.4
18	IA95032-6	IABG2C1	380.9	858.9	489.9	53.3	190.4	63.9	80.6	97.6
19	IA95029-4	IABG2C1	311.0	628.2	476.9	52.0	189.0	68.5	83.0	86.0
20	IA95029-3	IABG2C1	366.6	776.0	495.5	58.4	198.3	71.6	79.7	92.7
21	IA94192-7	IABG2C0	438.7	1003.6	485.1	43.2	206.3	67.8	81.6	100.5
22	IA94192-1	IABG2C0	462.5	1053.6	510.0	50.6	204.1	72.2	82.7	95.5
23	IA94190-10	IABG2C0	444.4	934.8	508.5	54.4	190.1	68.3	75.6	94.1
24	IA94190-1	IABG2C0	471.2	1003.3	493.9	57.1	185.7	68.4	75.7	95.6
25	IA94187-5	IABG2C0	318.7	727.8	493.2	48.4	198.6	59.5	81.6	89.7
26	IA94187-10	IABG2C0	414.8	852.3	507.0	45.0	190.4	66.5	76.6	89.2
27	IA94178-6	IABG2C0	415.1	877.4	519.6	54.3	173.0	68.2	81.9	94.1
28	IA94178-1	IABG2C0	435.5	951.7	504.7	53.5	176.6	60.5	82.6	96.6

Table 11. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set one evaluated in 1997 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
29	IA94163-6	IABG2C0	306.3	706.0	499.1	44.9	202.5	55.8	81.8	96.4
30	IA94163-3	IABG2C0	347.3	808.2	466.7	40.7	194.5	58.7	83.9	94.1
31	IA94143-7	IABG2C0	414.9	1049.8	495.3	41.1	185.6	79.3	77.1	100.4
32	IA94143-4	IABG2C0	446.7	966.3	474.6	51.8	190.7	75.9	83.5	93.6
33	IA94059-6	IABG2C0	323.7	692.2	491.7	46.2	206.3	69.8	79.5	90.2
34	IA94059-4	IABG2C0	330.5	751.3	468.3	40.8	207.3	68.0	83.0	92.1
35	IA94056-7	IABG2C0	352.8	819.2	464.2	46.1	208.7	59.3	81.7	97.1
36	IA94056-2	IABG2C0	283.0	758.2	467.6	.	.	.	82.0	100.5
37	IA94049-5	IABG2C0	432.7	962.7	467.1	43.2	210.1	66.2	81.0	95.5
38	IA94049-4	IABG2C0	502.1	1092.8	468.3	49.9	197.0	66.7	76.7	94.5
39	IA94031-7	IABG2C0	303.6	722.8	495.6	57.0	201.0	59.0	79.6	96.0
40	IA94031-6	IABG2C0	356.0	797.3	467.1	53.6	202.7	57.6	81.7	89.0
41	IA93150-5	IABGPI	431.0	932.7	499.6	49.8	195.3	63.5	79.2	102.8
42	IA93150-1	IABGPI	393.1	874.8	500.9	52.4	186.7	64.3	76.0	93.0
43	IA93108-5	IABG1C1	548.7	1085.7	492.1	51.2	177.1	59.8	81.7	96.3
44	IA93108-4	IABG1C1	356.1	777.2	486.3	47.8	195.5	59.4	82.3	94.8
45	IA93089-4	IABG1C1	590.3	1298.9	472.7	43.7	188.4	56.0	82.4	101.1
46	IA93089-1	IABG1C1	508.0	1082.4	519.6	43.2	188.2	63.9	83.5	101.1
47	IA93067-5	IABGPI	291.3	764.4	455.4	46.2	186.6	73.4	82.2	104.0
48	IA93067-2	IABGPI	422.9	981.4	485.2	49.3	189.7	75.0	76.0	106.1
49	IA93061-5	IABGPI	316.3	750.6	477.8	51.4	197.8	68.8	75.8	98.4
50	IA93061-3	IABGPI	285.2	704.7	450.2	38.6	198.5	77.7	82.6	93.7
51	IA93052-6	IABG1C1	222.8	652.5	.	44.8	213.8	63.6	82.5	90.5
52	IA93052-5	IABG1C1	291.5	836.8	513.3	.	.	.	79.0	103.3
53	IA93034-2	IABGPI	376.1	786.0	494.8	61.5	204.6	79.0	75.6	91.4
54	IA93034-1	IABGPI	445.1	912.9	496.3	53.0	198.5	76.1	76.8	89.9
55	IA93029-6	IABG1C1	334.8	832.7	487.4	55.4	180.9	55.8	80.7	97.9
56	IA93029-4	IABG1C1	447.1	912.6	473.3	53.6	179.8	68.7	81.8	95.6

Table 11. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set one evaluated in 1997 at

Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date day	Height cm
57	IA93028-3	IABGPI	397.5	937.6	480.1	41.4	200.1	70.8	83.7	102.0
58	IA93028-2	IABGPI	364.5	809.9	490.4	35.6	206.8	67.1	84.0	96.3
59	IA93014-3	IABGPI	377.0	891.6	490.7	54.0	194.2	68.0	77.6	99.2
60	IA93014-1	IABGPI	449.8	981.2	498.3	50.8	184.3	72.1	81.0	98.8
61	IA91509-4	IABGIC0	503.4	1059.2	451.7	46.4	185.7	61.2	83.0	100.8
62	IA91509-2	IABGIC0	382.9	883.0	490.0	45.6	196.8	64.4	82.7	99.9
63	IA91504-2	IABGIC0	396.6	966.4	492.0	45.3	172.4	78.8	83.1	101.6
64	IA91504-11	IABGIC0	439.8	1148.5	482.1	53.1	184.5	66.3	82.7	98.5
65	IA91500-8	IABGIC0	371.3	1109.7	460.6	42.2	182.6	68.5	83.4	111.4
66	IA91500-6	IABGIC0	335.8	897.0	501.0	47.8	184.7	73.7	81.9	102.7
67	IA91486-2	IABGIC0	336.4	832.2	505.2	49.4	192.8	56.3	80.7	97.9
68	IA91486-11	IABGIC0	323.7	881.2	497.9	49.4	186.9	56.9	80.9	101.2
69	IA91485-4	IABGIC0	541.3	1139.7	515.8	45.9	168.4	59.1	83.5	105.3
70	IA91485-18	IABGIC0	421.2	889.8	509.3	48.4	174.4	58.6	79.9	97.1
71	IA91479-6	IABGIC0	453.2	1051.7	505.6	31.5	171.2	67.4	81.2	104.0
72	IA91479-2	IABGIC0	333.8	726.0	467.9	37.4	188.6	66.4	82.5	110.6
73	IA91478-6	IABGIC0	369.1	957.4	543.4	40.1	186.9	60.7	75.9	104.0
74	IA91478-1	IABGIC0	458.2	997.0	500.8	37.8	179.8	66.0	78.9	98.8
75	IA91470-3	IABGIC0	463.7	1034.8	519.3	41.8	199.7	60.6	80.2	103.0
76	IA91470-10	IABGIC0	460.9	1028.3	482.3	51.6	193.5	57.0	80.6	100.9
77	IA91462-17	IABGIC0	422.7	978.2	497.4	40.7	188.4	70.1	83.5	103.8
78	IA91462-11	IABGIC0	328.6	950.3	503.3	44.7	189.8	72.0	81.2	104.9
79	IA91448-3	IABGIC0	400.8	994.6	461.7	35.0	199.9	66.9	83.5	104.5
80	IA91448-1	IABGIC0	508.8	1195.3	490.8	39.7	194.8	63.3	84.0	98.0
81	IL82-2154	Par. line	428.5	987.5	479.5	35.2	189.7	64.1	82.7	99.0
82	D831-1-571	Par. line	484.4	988.3	496.8	55.2	184.3	68.4	74.9	95.9
83	OA926-2	Par. line	338.2	855.4	479.8	39.8	181.8	64.7	83.2	114.4
84	P1412928	Par. line	367.2	903.2	464.2	50.0	203.1	52.7	80.5	104.4

Table 11. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set one evaluated in 1997 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	PI504593	Par. line	357.5	569.1	500.7	49.3	185.3	66.9	79.7	79.0
86	Hazel	Check	481.0	964.6	499.5	38.9	186.5	78.1	81.4	92.9
87	Hazel	Check	527.9	1047.5	491.2	36.4	183.1	79.2	79.5	91.3
88	Starter	Check	424.7	913.9	512.9	42.2	191.5	63.2	77.2	94.0
89	Starter	Check	371.9	833.2	.	49.0	192.9	60.1	77.5	93.9
90	Premier	Check	524.4	1095.8	546.7	59.1	181.3	60.2	80.5	96.7
91	Premier	Check	436.7	919.3	539.6	54.7	176.3	61.7	81.9	99.3
92	Marion	Check	541.4	1169.9	502.8	45.4	178.9	74.6	82.9	109.1
93	Marion	Check	543.6	1179.0	497.6	47.6	172.9	75.2	82.6	112.2
94	Noble	Check	288.0	716.4	499.2	43.3	205.0	60.0	81.9	96.8
95	Noble	Check	333.7	873.6	508.2	42.8	200.0	59.7	81.8	97.4
96	Ogle	Check	513.6	1056.0	476.6	41.7	179.5	59.2	80.1	95.6
97	Ogle	Check	493.1	1031.1	485.6	38.2	180.3	61.6	81.0	96.1
98	Don	Check	357.4	757.8	499.8	40.9	177.6	69.6	78.3	90.5
99	Don	Check	360.4	750.8	503.8	37.1	169.2	73.2	80.2	87.8
100	IAN979-5-2	Check	407.6	951.6	467.9	48.6	192.1	74.9	85.3	91.5
Mean [†]			396.4	895.1	502.2	50.2	179.1	66.8	86.7	80.9
LSD [‡]	Entry vs Entry		186.4	361.9	29.1	5.8	10.9	4.2	4.0	9.7

[†] Mean of all entries evaluated in 1997 at Ames.

[‡] Least significant difference at the 0.05 probability level.

Table 12. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set two evaluated in 1997 at Ames, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
	I									
1	A95196-7	IABG2C1	192.9	476.1	450.1	66.8	194.2	61.3	82.3	89.9
2	IA95196-5	IABG2C1	286.9	653.0	480.5	59.1	191.8	67.2	82.3	90.9
3	IA95189-9	IABG2C1	231.4	545.0	.	62.0	195.6	52.7	78.3	91.8
4	IA95189-2	IABG2C1	243.1	549.3	510.5	62.8	191.2	56.4	80.3	94.9
5	IA95181-6	IABG2C1	302.3	753.6	481.1	.	.	.	82.5	92.5
6	IA95181-4	IABG2C1	291.0	692.6	507.7	.	.	.	84.2	89.5
7	IA95172-4	IABG2C1	244.0	573.7	457.9	59.1	194.5	49.5	81.1	88.0
8	IA95172-1	IABG2C1	307.4	671.3	494.1	.	.	.	80.1	96.8
9	IA95148-3	IABG2C1	399.8	924.3	493.6	61.5	199.8	77.9	75.5	99.2
10	IA95148-1	IABG2C1	446.7	1049.3	491.4	57.9	190.0	79.6	77.9	100.7
11	IA95109-3	IABG2C1	548.3	1162.1	492.6	54.5	171.6	62.6	79.6	112.7
12	IA95109-2	IABG2C1	306.4	738.3	474.6	54.8	174.3	64.2	80.5	111.0
13	IA95103-6	IABG2C1	237.1	735.3	401.7	.	.	.	83.2	97.4
14	IA95103-3	IABG2C1	450.8	942.6	487.7	58.8	188.3	56.7	75.6	95.1
15	IA95038-9	IABG2C1	474.5	973.1	473.4	60.6	190.0	56.7	75.7	94.5
16	IA95038-7	IABG2C1	345.2	790.2	478.6	63.1	194.9	57.4	78.7	96.8
17	IA95032-9	IABG2C1	333.2	683.5	466.0	62.6	194.1	57.7	81.7	88.7
18	IA95032-6	IABG2C1	339.5	726.1	467.8	63.0	195.4	63.2	80.2	94.8
19	IA95029-4	IABG2C1	488.7	1012.7	521.8	62.5	184.0	68.2	82.1	95.6
20	IA95029-3	IABG2C1	340.8	742.3	518.9	58.0	176.6	61.9	82.4	92.7
21	IA94192-7	IABG2C0	373.9	863.3	509.8	53.6	193.4	69.1	83.4	100.5
22	IA94192-1	IABG2C0	562.8	1204.8	494.6	59.4	184.3	66.2	82.9	100.4
23	IA94190-10	IABG2C0	396.6	918.2	509.1	61.7	198.3	55.2	81.3	91.8
24	IA94190-1	IABG2C0	297.3	759.7	511.2	57.3	193.4	60.1	83.3	96.6
25	IA94187-5	IABG2C0	485.2	1021.9	503.2	64.5	188.5	77.4	74.2	97.4
26	IA94187-10	IABG2C0	381.5	930.4	504.1	57.0	193.9	74.3	74.9	103.1
27	IA94178-6	IABG2C0	324.1	713.9	501.7	59.4	201.2	50.0	76.1	92.3
28	IA94178-1	IABG2C0	314.9	771.9	507.2	.	.	.	74.5	89.6

Table 12. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set two evaluated in 1997 at

Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β -Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date day	Height cm
29	IA94163-6	IABG2C0	317.2	759.7	502.5	.	.	.	82.6	94.8
30	IA94163-3	IABG2C0	481.7	1018.8	502.4	57.7	180.4	74.2	82.2	89.0
31	IA94143-7	IABG2C0	247.5	893.8	407.9	.	.	.	82.8	90.1
32	IA94143-4	IABG2C0	386.5	866.4	474.0	61.6	201.3	60.8	81.0	96.8
33	IA94059-6	IABG2C0	479.5	1046.3	502.8	65.0	190.7	67.8	81.2	99.5
34	IA94059-4	IABG2C0	426.8	1016.9	497.6	57.2	180.8	62.8	79.3	96.4
35	IA94056-7	IABG2C0	373.3	909.1	481.2	52.2	204.8	57.1	82.0	101.2
36	IA94056-2	IABG2C0	236.6	645.9	398.4	.	.	.	78.0	99.8
37	IA94049-5	IABG2C0	530.0	1070.7	524.5	50.1	176.5	66.7	79.0	100.9
38	IA94049-4	IABG2C0	368.9	884.7	529.1	52.6	182.8	59.2	76.2	101.1
39	IA94031-7	IABG2C0	189.8	534.1	429.6	.	.	.	82.8	87.6
40	IA94031-6	IABG2C0	236.4	622.5	450.7	56.2	209.3	59.7	82.4	87.0
41	IA93150-5	IABG1C1	438.2	1085.9	505.6	54.1	199.0	57.0	81.0	99.0
42	IA93150-1	IABG1C1	422.9	1012.7	526.8	54.7	202.1	58.9	80.3	99.9
43	IA93108-5	IABG1C1	388.4	957.9	515.3	48.5	192.9	65.7	80.5	93.8
44	IA93108-4	IABG1C1	489.6	1046.3	490.9	52.9	196.8	55.9	81.3	94.3
45	IA93089-4	IABG1C1	571.3	1271.9	473.9	50.6	185.2	64.8	84.4	96.2
46	IA93089-1	IABG1C1	549.2	1223.1	489.2	54.6	182.9	56.4	82.4	97.2
47	IA93067-5	IABG1C1	559.0	1250.6	500.7	55.0	198.0	64.4	82.0	97.5
48	IA93067-2	IABG1C1	505.7	1143.8	507.8	51.4	198.2	68.0	80.9	104.6
49	IA93061-5	IABG1C1	472.3	997.5	483.3	55.1	182.0	57.2	82.9	96.9
50	IA93061-3	IABG1C1	422.5	1024.9	500.1	48.7	193.7	60.1	80.7	100.3
51	IA93052-6	IABG1C1	466.3	1024.9	505.4	55.6	188.3	75.3	74.1	96.2
52	IA93052-5	IABG1C1	431.0	927.4	508.8	53.9	197.3	76.8	74.5	97.9
53	IA93034-2	IABG1C1	589.9	1390.8	495.4	49.2	191.6	72.3	84.0	100.0
54	IA93034-1	IABG1C1	491.5	1073.7	506.1	50.0	189.7	67.4	81.3	96.5
55	IA93029-6	IABG1C1	281.2	744.4	469.8	52.1	208.1	58.1	78.9	94.2
56	IA93029-4	IABG1C1	376.7	884.7	482.7	47.0	207.6	61.6	77.9	94.8

Table 12. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set two evaluated in 1997 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
57	IA93028-3	IABG1C1	527.4	1137.8	494.6	46.3	170.2	65.9	81.6	98.4
58	IA93028-2	IABG1C1	462.2	1073.7	502.1	49.2	169.8	64.2	83.2	99.6
59	IA93014-3	IABG1C1	583.6	1207.9	501.3	51.6	173.5	71.4	76.4	94.9
60	IA93014-1	IABG1C1	400.7	985.3	522.4	52.9	185.5	63.5	76.0	94.7
61	IA91509-4	IABG1C0	392.2	933.5	504.9	43.6	167.2	66.1	84.2	111.1
62	IA91509-2	IABG1C0	367.9	988.4	484.6	44.0	176.3	68.1	82.3	107.9
63	IA91504-2	IABG1C0	339.2	945.7	508.4	46.3	183.2	62.1	83.5	104.7
64	IA91504-11	IABG1C0	265.5	820.7	491.0	42.9	194.5	62.7	83.6	107.4
65	IA91500-8	IABG1C0	338.9	997.5	487.4	40.7	207.4	74.8	87.0	109.6
66	IA91500-6	IABG1C0	378.3	1320.7	452.6	48.2	200.1	74.9	85.2	103.6
67	IA91486-2	IABG1C0	144.2	549.5	82.8	95.1
68	IA91486-11	IABG1C0	194.2	689.6	.	53.9	196.1	55.1	83.1	103.8
69	IA91485-4	IABG1C0	331.7	933.5	481.1	47.3	201.5	60.0	81.0	104.8
70	IA91485-18	IABG1C0	307.4	875.5	510.3	48.5	193.0	60.8	79.1	104.7
71	IA91479-6	IABG1C0	357.2	957.9	493.1	44.5	170.1	67.6	82.6	104.3
72	IA91479-2	IABG1C0	282.8	707.8	495.3	44.1	170.0	64.7	82.8	102.4
73	IA91478-6	IABG1C0	589.9	1165.2	492.4	51.2	193.2	70.7	82.3	101.7
74	IA91478-1	IABG1C0	530.9	1034.1	518.6	51.2	179.0	68.2	82.3	87.8
75	IA91470-3	IABG1C0	507.3	1284.1	459.5	51.0	197.1	67.7	84.7	102.3
76	IA91470-10	IABG1C0	299.5	1046.3	445.1	48.3	202.7	58.2	82.8	104.3
77	IA91462-17	IABG1C0	510.7	1146.9	488.2	48.4	193.9	68.4	81.5	98.9
78	IA91462-11	IABG1C0	476.4	1052.4	481.8	50.9	196.6	60.9	83.6	95.1
79	IA91448-3	IABG1C0	281.8	781.0	429.4	52.5	192.4	62.5	85.5	101.3
80	IA91448-1	IABG1C0	489.6	1122.5	509.3	47.7	201.7	68.1	81.8	102.1
81	H52-5	Par. line	483.3	1031.0	479.2	46.7	174.6	74.1	82.1	96.9
82	P7869D1-5 [†]	Par. line	440.4	994.5	.	49.1	195.4	60.5	80.1	100.2
83	NO5-1	Par. line	133.7	412.1	84.4	96.1
84	CO5406..380	Par. line	175.3	470.0	512.3	.	.	.	82.7	102.7

Table 12. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set two evaluated in 1997 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	PI504601	Par. line	349.3	781.0	533.2	49.1	200.5	73.2	79.0	94.6
86	Hazel	Check	537.5	1079.8	494.9	54.4	180.3	77.9	80.7	93.5
87	Hazel	Check	550.8	1125.6	504.7	54.1	177.8	80.0	82.0	93.9
88	Starter	Check	415.8	884.7	515.8	54.4	186.1	63.1	77.9	95.2
89	Starter	Check	341.4	805.4	498.1	48.9	183.0	61.9	80.1	97.7
90	Premier	Check	437.3	942.6	533.8	58.7	179.0	59.1	80.0	96.7
91	Premier	Check	442.3	881.6	516.9	57.2	167.9	59.5	81.3	96.5
92	Marion	Check	426.9	988.4	494.3	52.9	170.5	75.7	83.8	107.1
93	Marion	Check	517.4	1137.8	503.4	54.2	169.6	75.4	82.7	109.6
94	Noble	Check	303.1	768.0	499.6	50.1	205.2	58.4	82.9	97.2
95	Noble	Check	292.2	747.5	504.7	48.5	206.2	60.8	81.8	97.8
96	Ogle	Check	553.9	1134.7	459.0	47.4	170.9	60.4	81.0	97.7
97	Ogle	Check	461.9	945.7	484.6	48.2	180.6	58.3	81.1	96.8
98	Don	Check	460.0	1024.9	510.2	52.3	167.5	70.7	78.5	91.8
99	Don	Check	487.4	1031.0	505.2	47.6	165.0	73.0	78.5	91.8
100	IAN979-5-2	Check	356.3	832.9	475.3	60.6	189.5	75.2	83.8	93.5
Mean [†]			396.4	895.1	502.2	50.2	179.1	66.8	86.7	80.9
LSD [‡]	Entry vs Entry		186.4	361.9	29.1	5.8	10.9	4.2	4.0	9.7

[†] Mean of all entries evaluated in 1997 at Ames.

[‡] Least significant difference at the 0.05 probability level.

Table 13. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set three evaluated in 1997 at Ames, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
1	IA95196-7	IABG2C1	157.8	386.4	.	64.8	201.1	55.0	82.7	83.0
2	IA95196-5	IABG2C1	198.1	424.1	.	54.8	173.8	64.9	82.7	82.9
3	IA95189-9	IABG2C1	472.7	1045.3	489.4	60.7	198.2	80.8	78.6	102.4
4	IA95189-2	IABG2C1	391.2	811.4	514.9	62.7	194.2	68.1	74.6	94.0
5	IA95181-6	IABG2C1	519.3	1145.8	480.2	57.1	201.2	68.9	79.7	106.1
6	IA95181-4	IABG2C1	376.6	850.2	492.4	61.8	206.8	64.5	76.2	95.0
7	IA95172-4	IABG2C1	336.0	751.9	502.9	60.2	187.0	54.3	80.3	91.4
8	IA95172-1	IABG2C1	290.3	660.4	493.1	70.3	183.2	58.8	80.5	89.0
9	IA95148-3	IABG2C1	214.8	526.5	.	59.1	190.3	61.2	81.9	91.7
10	IA95148-1	IABG2C1	384.3	810.6	514.0	59.5	190.6	61.3	81.1	92.9
11	IA95109-3	IABG2C1	306.7	637.3	482.7	61.3	181.1	67.5	83.5	90.3
12	IA95109-2	IABG2C1	329.4	723.0	465.7	64.8	192.1	66.8	81.9	96.9
13	IA95103-6	IABG2C1	285.8	686.6	468.6	63.8	187.4	51.6	81.9	85.9
14	IA95103-3	IABG2C1	363.9	856.8	460.8	61.5	199.3	55.5	82.9	88.7
15	IA95038-9	IABG2C1	297.2	672.9	449.2	65.1	198.9	54.6	83.5	86.9
16	IA95038-7	IABG2C1	280.6	696.7	463.3	.	.	.	83.7	89.7
17	IA95032-9	IABG2C1	260.3	672.3	520.6	58.5	209.0	54.6	81.3	97.8
18	IA95032-6	IABG2C1	226.8	555.0	84.9	103.1
19	IA95029-4	IABG2C1	328.3	792.8	476.3	.	.	.	76.8	90.1
20	IA95029-3	IABG2C1	322.2	780.6	486.0	59.7	195.7	61.6	82.7	94.8
21	IA94192-7	IABG2C0	286.7	654.9	498.8	57.6	197.9	66.2	80.5	87.4
22	IA94192-1	IABG2C0	324.5	609.7	460.4	53.6	198.6	68.7	79.2	92.3
23	IA94190-10	IABG2C0	385.1	831.5	459.5	.	.	.	81.6	86.6
24	IA94190-1	IABG2C0	376.8	919.9	464.1	.	.	.	82.7	89.1
25	IA94187-5	IABG2C0	450.2	976.0	505.7	57.0	188.7	70.8	82.7	101.0
26	IA94187-10	IABG2C0	538.5	1143.3	487.1	56.5	181.0	73.7	82.7	107.1
27	IA94178-6	IABG2C0	354.0	800.6	470.2	65.9	203.3	48.8	79.7	86.3
28	IA94178-1	IABG2C0	380.3	810.8	487.7	61.5	199.4	47.4	83.7	87.8

Table 13. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set three evaluated in 1997 at

Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date day	Height cm
29	IA94163-6	IABG2C0	150.5	518.4		54.8	235.9	44.2	79.2	85.7
30	IA94163-3	IABG2C0	319.7	847.0	477.7	67.3	220.9	49.6	78.9	97.5
31	IA94143-7	IABG2C0	345.7	893.2	482.0	54.6	201.3	53.3	83.5	92.0
32	IA94143-4	IABG2C0	295.2	727.6	510.7	53.8	204.6	59.0	82.4	96.0
33	IA94059-6	IABG2C0	285.3	691.0	453.4	53.6	195.9	61.8	84.3	93.3
34	IA94059-4	IABG2C0	357.1	754.1	450.4	51.0	190.1	62.3	82.7	92.3
35	IA94056-7	IABG2C0	239.8	555.6	458.1	58.0	202.1	54.8	80.5	86.7
36	IA94056-2	IABG2C0	498.7	1043.5	502.2				80.3	105.0
37	IA94049-5	IABG2C0	324.5	712.8	466.1	57.6	190.2	63.6	85.1	85.8
38	IA94049-4	IABG2C0	329.5	668.1	459.4	63.0	181.2	61.0	81.9	84.4
39	IA94031-7	IABG2C0	454.2	887.4	491.1	54.3	178.7	61.7	82.7	88.3
40	IA94031-6	IABG2C0	429.0	881.1	478.2	65.5	183.1	64.9	79.7	85.8
41	IA93150-5	IABG1C1	451.6	1024.7	465.9	58.3	196.2	67.5	80.3	99.8
42	IA93150-1	IABG1C1	414.9	1008.2	509.4	56.7	192.6	65.9	80.5	96.3
43	IA93108-5	IABGPI	449.5	927.5	433.9				81.3	93.8
44	IA93108-4	IABGPI	487.0	977.4	450.0	51.8	191.5	77.9	81.9	90.9
45	IA93089-4	IABGPI	523.8	1120.9	482.3	51.5	177.1	71.9	77.0	105.1
46	IA93089-1	IABGPI	488.4	1049.2	473.3	52.1	182.2	70.8	82.7	105.0
47	IA93067-5	IABG1C1	473.8	1049.1	489.4	49.9	185.5	61.7	82.7	96.0
48	IA93067-2	IABG1C1	486.5	1044.7	467.4	60.2	190.4	55.8	77.0	88.8
49	IA93061-5	IABG1C1	448.2	958.6	485.7	55.9	194.8	69.3	82.7	95.7
50	IA93061-3	IABG1C1	432.7	946.7	459.5	57.9	187.6	69.8	81.9	97.1
51	IA93052-6	IABG1C1	455.1	955.8	456.3	68.3	180.7	70.4	77.0	91.8
52	IA93052-5	IABG1C1	517.3	1066.7	485.8	62.0	174.4	68.9	79.7	92.7
53	IA93034-2	IABG1C1	418.6	991.5	484.3	66.7	192.1	69.6	83.5	91.8
54	IA93034-1	IABG1C1	421.5	878.2	515.4	68.3	190.8	69.2	78.6	93.3
55	IA93029-6	IABGPI	480.7	1113.2	465.4	54.0	180.6	66.0	84.3	107.1
56	IA93029-4	IABGPI	308.1	859.8	422.4	49.5	178.4	66.1	81.1	112.9

Table 13. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set three evaluated in 1997 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
57	IA93028-3	IABGPI	482.5	1042.1	443.9	52.6	200.6	76.5	75.7	101.6
58	IA93028-2	IABGPI	420.7	1041.7	452.4	58.8	191.9	75.9	81.1	100.1
59	IA93014-3	IABG1C1	516.3	1068.2	443.7	54.8	177.7	65.2	82.7	97.1
60	IA93014-1	IABG1C1	526.7	1065.5	480.7	.	.	.	81.9	95.7
61	IA91509-4	IABG1C0	367.7	728.6	478.3	55.3	175.5	76.1	81.9	92.0
62	IA91509-2	IABG1C0	444.6	937.2	491.6	49.9	193.6	74.9	82.7	102.2
63	IA91504-2	IABG1C0	276.3	716.1	517.8	52.5	197.0	65.1	77.0	95.7
64	IA91504-11	IABG1C0	477.3	960.4	517.9	43.0	171.0	59.8	80.3	101.9
65	IA91500-8	IABG1C0	295.3	854.9	510.6	53.1	187.6	67.7	80.3	100.7
66	IA91500-6	IABG1C0	395.6	1082.1	501.9	50.6	177.1	59.6	82.7	106.6
67	IA91486-2	IABG1C0	520.4	982.3	503.2	42.0	167.8	71.6	81.1	101.4
68	IA91486-11	IABG1C0	359.0	857.3	527.1	42.4	183.3	73.0	79.2	101.2
69	IA91485-4	IABG1C0	311.6	712.9	510.9	50.5	168.2	75.8	79.2	101.1
70	IA91485-18	IABG1C0	371.9	964.2	479.7	42.3	183.1	74.9	85.1	94.5
71	IA91479-6	IABG1C0	324.7	846.0	488.8	45.8	187.1	63.3	82.9	108.0
72	IA91479-2	IABG1C0	423.2	886.5	482.7	45.5	173.4	67.4	79.7	100.1
73	IA91478-6	IABG1C0	498.9	1057.2	499.1	57.1	180.4	72.3	80.5	102.2
74	IA91478-1	IABG1C0	324.2	733.0	511.3	53.4	188.4	69.5	84.3	103.4
75	IA91470-3	IABG1C0	435.1	960.0	487.5	47.6	167.7	64.6	80.3	97.3
76	IA91470-10	IABG1C0	460.6	979.5	469.0	.	.	.	81.9	99.5
77	IA91462-17	IABG1C0	329.0	798.9	467.1	56.5	199.6	74.8	83.5	90.1
78	IA91462-11	IABG1C0	408.8	848.7	479.2	58.5	181.2	75.2	78.9	94.7
79	IA91448-3	IABG1C0	505.7	1199.5	509.9	50.8	179.5	55.8	81.9	105.0
80	IA91448-1	IABG1C0	482.9	1060.0	470.2	47.8	175.4	62.0	83.5	102.2
81	H87-7-4	Par. line	476.9	1106.6	501.5	.	.	.	83.2	100.7
82	MO07929	Par. line	569.2	1181.1	450.8	52.7	190.1	80.7	85.1	96.7
83	MN88156	Par. line	286.9	675.3	462.3	52.7	203.7	53.5	81.6	98.1
84	NO4-8	Par. line	179.1	452.4	82.6	84.9

Table 13. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set three evaluated in 1997 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	PI361884	Par. line	391.9	852.3	470.1	43.4	167.8	74.5	83.5	105.1
86	Hazel	Check	502.3	996.1	486.5	54.6	177.1	79.8	81.1	93.2
87	Hazel	Check	466.3	949.1	495.2	51.7	181.6	78.3	81.9	91.3
88	Starter	Check	351.1	747.9	509.7	50.1	182.0	65.8	78.4	93.3
89	Starter	Check	393.3	865.2	519.8	53.4	189.9	65.3	78.4	97.1
90	Premier	Check	434.8	892.3	527.8	53.6	174.4	58.4	81.9	96.2
91	Premier	Check	367.0	810.0	528.3	56.7	175.3	60.3	81.1	96.0
92	Marion	Check	468.7	1033.9	481.5	53.8	167.4	73.1	82.7	110.4
93	Marion	Check	563.7	1260.4	477.7	57.3	169.9	75.1	82.7	114.2
94	Noble	Check	266.2	674.9	485.3	51.2	204.9	57.2	81.9	95.0
95	Noble	Check	369.8	855.4	508.7	49.7	198.1	59.7	81.1	96.3
96	Ogle	Check	515.0	1010.5	466.8	44.2	172.2	58.3	81.9	93.4
97	Ogle	Check	369.1	772.4	488.3	42.5	168.7	63.0	83.2	93.8
98	Don	Check	447.7	891.3	512.4	52.8	160.5	73.8	78.6	89.9
99	Don	Check	355.9	743.0	502.6	55.1	159.8	74.5	78.4	87.6
100	IAN979-5-2	Check	377.1	843.2	487.1	62.6	187.0	72.6	85.1	94.0
Mean [†]			396.4	895.1	502.2	50.2	179.1	66.8	86.7	80.9
LSD [‡]	Entry vs Entry		186.4	361.9	29.1	5.9	10.9	4.2	4.0	9.7

[†] Mean of all entries evaluated in 1997 at Ames.

[‡] Least significant difference at the 0.05 probability level.

Table 14. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set four evaluated in 1997 at Ames, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
1	IA95196-7	IABG2C1	299.7	660.0	486.9	46.6	175.0	69.4	83.2	82.4
2	IA95196-5	IABG2C1	353.3	765.9	472.6	58.3	199.3	60.2	80.2	96.1
3	IA95189-9	IABG2C1	260.7	582.2	503.4	60.6	207.5	64.2	83.9	92.3
4	IA95189-2	IABG2C1	353.3	851.6	484.4	62.5	215.6	66.2	80.4	94.2
5	IA95181-6	IABG2C1	214.9	505.8	445.6	67.4	222.9	59.9	79.6	79.9
6	IA95181-4	IABG2C1	343.4	766.4	474.9	58.8	211.8	57.2	79.6	89.2
7	IA95172-4	IABG2C1	255.0	753.3	408.2	58.4	220.8	60.5	83.0	102.9
8	IA95172-1	IABG2C1	448.5	1172.2	495.5	57.2	196.2	71.1	81.3	104.1
9	IA95148-3	IABG2C1	434.7	960.5	488.1	61.1	189.7	69.5	81.2	99.2
10	IA95148-1	IABG2C1	414.7	960.5	501.3	61.1	193.0	69.1	83.1	101.6
11	IA95109-3	IABG2C1	177.7	463.0	88.1	75.6
12	IA95109-2	IABG2C1	219.5	478.7	85.5	90.4
13	IA95103-6	IABG2C1	302.9	686.9	452.2	51.3	184.9	65.9	85.4	89.2
14	IA95103-3	IABG2C1	360.0	838.1	463.7	53.4	192.6	68.6	82.6	104.1
15	IA95038-9	IABG2C1	283.5	656.9	454.9	55.7	193.0	57.3	82.0	98.5
16	IA95038-7	IABG2C1	257.6	570.1	456.6	60.0	198.2	62.6	82.7	96.7
17	IA95032-9	IABG2C1	291.3	687.9	448.2	61.2	193.7	60.4	82.5	86.1
18	IA95032-6	IABG2C1	296.7	567.6	475.3	63.8	194.2	58.8	84.5	89.2
19	IA95029-4	IABG2C1	238.3	609.5	432.2	63.9	228.2	54.5	84.0	76.2
20	IA95029-3	IABG2C1	176.5	473.0	.	67.4	226.7	50.5	83.8	81.8
21	IA94192-7	IABG2C0	337.9	672.1	476.9	66.0	180.8	65.6	76.4	85.5
22	IA94192-1	IABG2C0	378.6	874.4	476.2	63.0	178.4	71.8	80.4	90.5
23	IA94190-10	IABG2C0	509.7	1061.8	512.7	.	.	.	76.0	94.2
24	IA94190-1	IABG2C0	274.3	710.9	483.0	57.3	203.3	51.4	80.8	93.6
25	IA94187-5	IABG2C0	440.2	1026.4	483.4	65.8	187.0	75.5	78.1	95.4
26	IA94187-10	IABG2C0	503.9	1160.2	495.4	57.4	190.4	68.8	81.2	95.4
27	IA94178-6	IABG2C0	314.2	643.1	482.8	66.2	179.8	75.1	81.3	86.1
28	IA94178-1	IABG2C0	431.1	919.0	498.3	61.2	176.0	77.4	83.4	95.4

Table 14. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set four evaluated in 1997 at

Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
29	IA94163-6	IABG2C0	483.7	1064.2	504.9	54.2	176.1	69.1	79.1	92.3
30	IA94163-3	IABG2C0	380.9	839.3	522.9	58.4	183.2	69.0	77.5	94.8
31	IA94143-7	IABG2C0	226.6	598.9	449.6	67.4	214.0	47.7	80.6	94.2
32	IA94143-4	IABG2C0	209.5	529.9	391.9	.	.	.	83.2	88.0
33	IA94059-6	IABG2C0	447.9	925.1	475.2	62.1	187.3	66.2	77.6	94.8
34	IA94059-4	IABG2C0	373.9	855.4	437.9	63.0	217.5	58.5	78.4	93.6
35	IA94056-7	IABG2C0	325.6	740.0	489.4	57.7	196.3	59.9	79.7	96.1
36	IA94056-2	IABG2C0	341.8	808.7	446.9	53.5	197.2	59.3	82.3	93.0
37	IA94049-5	IABG2C0	282.8	840.4	520.6	46.5	220.9	62.2	81.4	99.8
38	IA94049-4	IABG2C0	237.5	752.7	497.4	52.7	206.6	64.0	83.1	103.5
39	IA94031-7	IABG2C0	313.7	829.8	500.3	54.3	193.9	56.5	82.8	91.7
40	IA94031-6	IABG2C0	474.8	1089.6	500.1	50.8	189.9	61.5	83.6	95.4
41	IA93150-5	IABGPI	481.9	1057.6	432.1	49.3	176.3	72.1	82.6	103.5
42	IA93150-1	IABGPI	347.5	876.7	438.1	51.1	185.1	65.8	80.7	109.7
43	IA93108-5	IABG1C1	412.0	1126.9	508.2	48.7	200.6	73.2	81.5	104.7
44	IA93108-4	IABG1C1	563.6	1228.9	496.3	59.3	195.7	80.3	79.8	101.0
45	IA93089-4	IABG1C1	436.1	1007.6	508.9	55.5	193.2	59.9	80.5	103.2
46	IA93089-1	IABG1C1	536.6	1183.3	507.6	49.9	194.6	63.9	80.9	103.5
47	IA93067-5	IABGPI	484.3	1034.6	478.2	54.0	174.2	76.0	80.6	96.7
48	IA93067-2	IABGPI	463.8	966.1	470.6	60.6	179.4	67.8	79.8	94.8
49	IA93061-5	IABGPI	333.7	735.4	400.9	55.2	174.6	74.6	75.7	96.7
50	IA93061-3	IABGPI	530.0	1110.5	474.5	52.5	182.4	75.8	80.4	94.2
51	IA93052-6	IABG1C1	464.1	1017.8	492.8	62.3	181.1	63.9	82.4	100.4
52	IA93052-5	IABG1C1	498.2	1107.3	511.5	59.7	190.8	59.8	81.3	101.0
53	IA93034-2	IABGPI	445.8	1004.3	477.8	62.5	199.6	62.9	83.7	93.0
54	IA93034-1	IABGPI	486.8	1055.6	503.0	60.9	201.2	62.5	82.7	93.6
55	IA93029-6	IABGPI	561.9	1231.7	479.9	.	.	.	83.2	110.3
56	IA93029-4	IABGPI	434.7	965.9	544.1	51.4	194.6	72.0	82.7	101.6

Table 14. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set four evaluated in 1997 at

Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
57	IA93028-3	IABGPI	196.4	394.0	82.9	99.3
58	IA93028-2	IABGPI	195.7	603.0	449.8	57.9	213.1	57.3	82.8	85.5
59	IA93014-3	IABGIC1	470.0	988.1	496.1	48.9	178.2	71.0	76.1	92.3
60	IA93014-1	IABGIC1	433.2	916.7	469.4	53.5	192.7	60.9	77.0	91.7
61	IA91509-4	IABGIC0	389.8	890.5	477.2	52.0	180.5	66.7	84.0	91.7
62	IA91509-2	IABGIC0	494.8	1197.3	468.7	.	.	.	82.5	93.6
63	IA91504-2	IABGIC0	509.0	990.1	528.8	41.5	169.8	62.8	82.0	108.4
64	IA91504-11	IABGIC0	335.6	756.3	499.2	39.4	171.0	65.8	84.3	102.9
65	IA91500-8	IABGIC0	453.0	1115.3	490.4	51.4	173.3	71.4	81.1	104.7
66	IA91500-6	IABGIC0	357.8	946.4	496.3	.	.	.	81.2	102.9
67	IA91486-2	IABGIC0	482.8	1091.5	505.2	48.9	176.5	69.4	84.1	112.2
68	IA91486-11	IABGIC0	524.3	1191.9	506.3	44.8	158.7	61.7	82.7	102.9
69	IA91485-4	IABGIC0	331.9	742.7	496.9	41.6	167.7	58.6	84.5	107.8
70	IA91485-18	IABGIC0	300.3	734.4	506.0	42.5	157.7	66.8	85.8	107.2
71	IA91479-6	IABGIC0	583.7	1237.0	516.5	51.4	177.2	60.7	81.9	102.9
72	IA91479-2	IABGIC0	434.5	922.8	497.7	49.4	176.2	72.6	82.8	99.2
73	IA91478-6	IABGIC0	471.7	977.8	502.4	57.7	180.9	65.7	81.0	97.3
74	IA91478-1	IABGIC0	498.5	1056.9	490.0	47.9	178.4	62.8	82.7	100.4
75	IA91470-3	IABGIC0	452.5	1076.8	498.4	47.1	193.5	61.2	79.9	103.5
76	IA91470-10	IABGIC0	480.4	1125.9	481.3	53.8	191.1	58.3	81.7	97.3
77	IA91462-17	IABGIC0	516.9	1156.1	487.8	54.4	192.0	60.0	80.6	93.6
78	IA91462-11	IABGIC0	534.8	1062.1	508.6	.	.	.	79.7	93.0
79	IA91448-3	IABGIC0	469.0	975.0	480.4	55.1	186.9	60.7	77.9	102.2
80	IA91448-1	IABGIC0	513.2	1111.8	469.2	50.1	174.3	72.8	84.8	104.1
81	H730-12	Par. line	318.3	709.6	437.9	56.4	203.0	57.6	83.7	102.9
82	MN86226	Par. line	316.9	841.9	503.9	52.0	209.5	71.3	81.3	100.4
83	NO20-1	Par. line	182.6	400.5	82.6	107.8
84	PI361886	Par. line	269.0	623.1	452.1	47.6	174.1	76.7	90.3	119.6

Table 14. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set four evaluated in 1997 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	PI502955	Par. line	366.2	821.3	488.2	63.5	194.0	73.0	74.5	101.6
86	Hazel	Check	414.0	898.7	502.2	.	.	.	81.4	89.9
87	Hazel	Check	473.0	945.0	498.7	53.1	175.7	80.2	80.7	92.3
88	Starter	Check	415.2	859.7	505.1	50.5	183.8	63.8	78.8	94.2
89	Starter	Check	478.4	1012.1	514.6	54.3	179.3	65.7	77.9	95.4
90	Premier	Check	422.1	906.5	542.0	58.3	179.5	58.1	81.4	94.8
91	Premier	Check	474.6	988.8	553.3	61.6	168.7	61.1	80.1	95.4
92	Marion	Check	557.7	1222.2	485.7	57.2	165.0	74.1	82.8	112.2
93	Marion	Check	398.4	955.1	459.7	56.9	171.9	74.2	83.8	108.4
94	Noble	Check	376.1	900.0	508.1	49.1	201.6	60.8	81.3	96.7
95	Noble	Check	291.6	701.0	510.0	49.1	206.1	58.8	81.1	96.1
96	Ogle	Check	353.3	985.6	483.7	39.8	169.1	62.4	82.0	96.7
97	Ogle	Check	445.5	905.8	457.4	44.2	167.7	62.2	82.0	96.1
98	Don	Check	375.5	756.3	489.2	53.2	162.6	72.5	80.0	88.0
99	Don	Check	434.6	902.3	498.2	55.2	159.9	74.3	78.3	88.6
100	IAN979-5-2	Check	507.7	1139.5	476.3	58.2	190.2	74.0	83.8	89.9
Mean†			396.4	895.1	502.2	50.2	179.1	66.8	86.7	80.9
LSD‡	Entry vs Entry		186.4	361.9	29.1	5.8	10.9	4.2	4.0	9.7

† Mean of all entries evaluated in 1997 at Ames.

‡ Least significant difference at the 0.05 probability level.

Table 15. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set five evaluated in 1997 at Ames, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
1	IA95196-7	IABG2C1	408.7	891.8	498.3	66.7	188.6	77.6	74.5	95.3
2	IA95196-5	IABG2C1	308.2	663.5	510.3	68.4	198.2	69.2	75.1	90.5
3	IA95189-9	IABG2C1	410.5	876.1	486.9	58.0	177.7	61.0	82.7	85.7
4	IA95189-2	IABG2C1	375.2	784.8	489.7	56.0	183.3	59.3	83.6	85.1
5	IA95181-6	IABG2C1	317.2	720.8	472.3	57.8	187.9	63.5	78.5	96.5
6	IA95181-4	IABG2C1	364.2	744.8	518.9	52.2	194.5	67.6	81.6	95.3
7	IA95172-4	IABG2C1	318.4	648.2	506.6	.	.	.	80.1	92.3
8	IA95172-1	IABG2C1	300.4	650.3	467.6	.	.	.	83.2	86.9
9	IA95148-3	IABG2C1	354.4	747.3	470.1	58.4	197.1	64.6	82.8	92.3
10	IA95148-1	IABG2C1	385.6	803.7	484.3	56.1	190.6	61.2	85.2	95.3
11	IA95109-3	IABG2C1	331.8	699.2	477.3	.	.	.	81.8	88.7
12	IA95109-2	IABG2C1	391.6	837.1	498.7	60.8	196.1	63.1	78.9	92.3
13	IA95103-6	IABG2C1	307.2	724.1	426.3	62.9	210.7	54.1	83.4	89.9
14	IA95103-3	IABG2C1	318.8	705.9	474.2	62.0	201.7	62.1	84.5	89.9
15	IA95038-9	IABG2C1	377.0	786.3	486.3	62.5	192.6	75.7	82.9	92.9
16	IA95038-7	IABG2C1	421.7	921.4	490.9	62.3	191.2	68.7	81.1	92.9
17	IA95032-9	IABG2C1	355.8	770.5	522.8	62.8	179.0	68.2	75.7	95.3
18	IA95032-6	IABG2C1	427.0	886.1	495.2	64.8	183.5	69.8	76.6	98.9
19	IA95029-4	IABG2C1	323.3	517.0	426.7	.	.	.	84.5	80.9
20	IA95029-3	IABG2C1	354.1	572.9	479.1	59.2	201.6	63.8	83.6	80.9
21	IA94192-7	IABG2C0	408.0	881.9	523.6	59.7	216.5	58.8	77.1	94.1
22	IA94192-1	IABG2C0	409.8	752.5	494.6	61.5	196.2	65.0	79.5	98.3
23	IA94190-10	IABG2C0	339.3	784.8	465.5	61.3	195.2	76.7	73.8	98.3
24	IA94190-1	IABG2C0	415.3	952.3	472.6	63.3	196.5	78.4	75.0	97.1
25	IA94187-5	IABG2C0	382.8	1137.5	469.3	56.9	190.0	58.1	83.5	95.3
26	IA94187-10	IABG2C0	400.9	1058.9	459.4	57.6	193.6	61.6	84.5	101.3
27	IA94178-6	IABG2C0	414.9	905.6	524.3	66.0	199.1	61.0	76.5	86.3
28	IA94178-1	IABG2C0	352.5	829.3	507.3	60.9	200.2	59.6	80.3	91.7

Table 15. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set five evaluated in 1997 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
29	IA94163-6	IABG2C0	439.9	871.9	524.9	52.5	195.7	63.7	80.1	94.1
30	IA94163-3	IABG2C0	428.8	1013.6	516.4	63.5	195.0	70.8	82.5	91.1
31	IA94143-7	IABG2C0	387.6	843.1	500.7	53.0	193.4	62.9	79.6	95.3
32	IA94143-4	IABG2C0	445.8	1024.6	510.7	52.8	194.1	62.9	81.2	95.3
33	IA94059-6	IABG2C0	376.3	778.5	495.0	57.7	201.4	58.1	79.5	82.7
34	IA94059-4	IABG2C0	432.0	916.4	500.2	56.9	203.2	52.1	78.3	86.3
35	IA94056-7	IABG2C0	423.0	917.2	483.2	56.2	201.1	62.5	81.1	98.9
36	IA94056-2	IABG2C0	496.9	1073.3	460.8	57.1	184.4	67.0	80.4	95.9
37	IA94049-5	IABG2C0	501.3	1122.6	495.9	55.0	186.9	62.2	79.0	98.3
38	IA94049-4	IABG2C0	452.6	979.9	471.8	50.9	184.5	61.0	79.6	93.5
39	IA94031-7	IABG2C0	355.4	733.3	520.6	57.2	194.7	60.9	79.0	94.7
40	IA94031-6	IABG2C0	482.8	1004.0	478.9	61.7	179.3	59.5	79.6	95.3
41	IA93150-5	IABG1C1	492.0	1110.7	472.8	56.3	197.9	63.5	82.7	101.3
42	IA93150-1	IABG1C1	458.3	960.0	487.9	53.4	184.8	60.3	80.2	96.5
43	IA93108-5	IABG1C1	428.4	741.2	508.0	53.5	196.0	63.6	83.1	99.5
44	IA93108-4	IABG1C1	463.2	1215.7	444.4	53.9	201.3	62.5	83.3	97.7
45	IA93089-4	IABG1C1	429.7	949.9	502.2	52.7	203.9	66.3	73.8	95.3
46	IA93089-1	IABG1C1	345.6	736.4	489.4	53.5	208.9	55.9	74.6	91.1
47	IA93067-5	IABG1C1	377.0	871.8	529.6	50.5	195.8	66.2	75.8	94.1
48	IA93067-2	IABG1C1	470.9	1168.1	603.6	55.2	197.7	67.9	77.2	96.5
49	IA93061-5	IABG1C1	432.7	1231.9	611.7	51.7	198.1	63.1	81.1	98.3
50	IA93061-3	IABG1C1	432.1	1033.6	511.7	52.3	196.5	70.5	80.0	100.1
51	IA93052-6	IABG1C1	402.0	832.7	461.2	55.8	212.5	67.2	77.1	98.9
52	IA93052-5	IABG1C1	327.8	786.7	455.9	52.7	226.7	64.0	81.9	98.9
53	IA93034-2	IABGPI	398.1	929.6	425.4	52.5	193.9	77.5	78.0	85.1
54	IA93034-1	IABGPI	433.3	933.7	454.1	54.7	197.4	74.2	81.9	87.5
55	IA93029-6	IABGPI	275.1	554.4	82.7	98.9
56	IA93029-4	IABGPI	375.8	895.4	454.4	49.1	188.0	59.8	80.7	100.1

Table 15. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set five evaluated in 1997 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
57	IA93028-3	IABG1C1	522.8	1150.7	503.4	62.1	172.3	68.9	81.1	100.1
58	IA93028-2	IABG1C1	444.5	934.2	503.9	58.3	173.5	72.0	79.3	101.9
59	IA93014-3	IABGPI	454.3	1145.4	462.9	45.4	191.9	74.0	83.0	106.4
60	IA93014-1	IABGPI	481.1	1330.2	470.2	46.1	186.4	72.9	82.0	113.3
61	IA91509-4	IABG1C0	440.4	938.5	438.8	51.8	170.7	65.3	82.7	88.7
62	IA91509-2	IABG1C0	500.0	1071.3	470.9	47.7	171.7	60.9	82.9	90.5
63	IA91504-2	IABG1C0	369.5	864.4	504.2	46.6	174.4	73.5	79.7	101.6
64	IA91504-11	IABG1C0	306.8	765.4	504.8	50.9	187.7	73.9	79.5	100.4
65	IA91500-8	IABG1C0	322.6	787.6	500.4	49.3	195.6	65.6	82.7	97.7
66	IA91500-6	IABG1C0	362.1	864.9	534.7	50.9	188.5	68.6	79.0	91.1
67	IA91486-2	IABG1C0	481.7	1058.6	481.8	51.8	186.7	67.4	81.0	101.9
68	IA91486-11	IABG1C0	450.2	1072.4	486.1	62.3	194.4	64.3	80.3	94.7
69	IA91485-4	IABG1C0	481.3	1079.9	489.6	44.1	187.5	54.3	82.6	101.3
70	IA91485-18	IABG1C0	415.3	900.4	496.9	44.3	179.7	65.0	81.8	94.1
71	IA91479-6	IABG1C0	411.5	972.8	514.5	53.9	193.6	67.0	79.8	95.9
72	IA91479-2	IABG1C0	445.2	1112.8	460.1	47.1	186.7	63.8	83.1	97.7
73	IA91478-6	IABG1C0	414.4	981.3	493.6	52.3	187.4	63.4	75.7	91.7
74	IA91478-1	IABG1C0	404.1	909.9	528.7	49.6	193.1	63.0	77.5	94.1
75	IA91470-3	IABG1C0	406.4	1053.3	512.8	44.6	191.9	62.5	80.1	97.1
76	IA91470-10	IABG1C0	379.9	1026.3	428.1	52.6	218.1	64.9	80.9	101.9
77	IA91462-17	IABG1C0	494.7	1218.3	471.6	.	.	.	85.1	103.1
78	IA91462-11	IABG1C0	505.2	1102.4	519.9	48.3	174.9	68.2	77.5	98.3
79	IA91448-3	IABG1C0	450.3	1032.0	497.3	60.9	176.1	72.7	81.0	100.1
80	IA91448-1	IABG1C0	404.9	885.7	506.2	60.6	181.7	71.6	76.9	98.9
81	H688-11	Par. line	481.9	1033.4	471.4	48.2	175.2	72.4	79.5	94.1
82	IL85-6183-1	Par. line	407.4	909.1	482.3	49.5	193.5	63.0	85.6	86.9
83	D921-255	Par. line	479.2	992.6	478.2	48.7	167.8	77.7	75.1	92.9
84	NO10-1	Par. line	406.0	907.3	80.4	94.8

Table 15. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set five evaluated in 1997 at Ames, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	NO11-1	Par. line	344.0	707.2	83.8	85.6
86	Hazel	Check	476.4	1007.9	484.3	50.1	175.2	79.1	80.0	89.9
87	Hazel	Check	437.9	895.5	494.7	48.8	169.1	78.8	80.0	87.5
88	Starter	Check	404.0	890.6	510.1	56.3	188.9	63.1	77.8	93.5
89	Starter	Check	351.9	831.1	511.8	53.7	192.2	67.5	80.4	93.5
90	Premier	Check	385.0	864.8	541.3	53.1	168.5	60.6	81.0	95.9
91	Premier	Check	397.0	859.1	521.6	54.1	176.3	57.8	81.9	95.3
92	Marion	Check	521.6	1190.7	490.1	54.1	166.1	74.8	82.7	110.9
93	Marion	Check	492.2	1123.6	505.1	51.7	168.9	72.7	83.6	111.5
94	Noble	Check	344.1	797.3	521.8	49.6	210.2	57.3	79.8	95.3
95	Noble	Check	331.7	777.7	521.6	49.6	207.7	57.9	81.9	95.3
96	Ogle	Check	385.4	896.9	476.2	42.4	177.1	58.0	82.7	94.7
97	Ogle	Check	432.6	898.6	478.3	42.3	169.5	59.1	81.9	94.7
98	Don	Check	347.3	708.1	485.6	50.6	168.1	72.3	80.0	90.2
99	Don	Check	381.2	785.1	523.9	50.8	162.4	72.4	79.0	88.7
100	IAN979-5-2	Check	406.9	905.3	481.1	58.5	190.3	71.7	84.8	90.5
Mean [†]			396.4	895.1	502.2	50.2	179.1	66.8	86.7	80.9
LSD [‡]	Entry vs Entry		186.4	361.9	29.1	5.8	10.9	4.2	4.0	9.7

[†] Mean of all entries evaluated in 1997 at Ames.

[‡] Least significant difference at the 0.05 probability level.

Table 16. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set one evaluated in 1997 at Nashua, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
1	IA95196-7	IABG2C1	326.4	808.4	459.4	57.0	171.7	78.9	.	.
2	IA95196-5	IABG2C1	409.5	981.4	477.7	56.0	170.1	79.4	.	.
3	IA95189-9	IABG2C1	143.5	457.2	.	58.1	204.2	59.5	.	.
4	IA95189-2	IABG2C1	243.7	596.6	441.6	58.0	187.6	65.7	.	.
5	IA95181-6	IABG2C1	199.4	470.2
6	IA95181-4	IABG2C1	287.9	703.1	477.4	56.0	191.0	65.8	.	.
7	IA95172-4	IABG2C1	241.7	642.4	457.8
8	IA95172-1	IABG2C1	307.3	758.6	484.2	67.7	187.2	75.1	.	.
9	IA95148-3	IABG2C1	264.4	673.3	476.6	59.1	175.1	67.4	.	.
10	IA95148-1	IABG2C1	232.2	637.7	467.7
11	IA95109-3	IABG2C1	234.6	614.4	.	62.2	176.3	62.2	.	.
12	IA95109-2	IABG2C1	308.5	727.5	446.9	64.9	165.5	71.6	.	.
13	IA95103-6	IABG2C1	306.0	706.2	486.1	57.2	193.6	74.1	.	.
14	IA95103-3	IABG2C1	334.5	854.0	485.6	56.9	183.3	73.2	.	.
15	IA95038-9	IABG2C1	411.1	920.9	486.2	52.4	170.7	63.5	.	.
16	IA95038-7	IABG2C1	315.4	813.6	474.4	52.7	171.6	62.1	.	.
17	IA95032-9	IABG2C1	242.5	584.5	454.2	58.5	171.8	73.9	.	.
18	IA95032-6	IABG2C1	273.6	713.5	459.3	58.3	179.3	69.7	.	.
19	IA95029-4	IABG2C1	224.7	546.9	434.6	60.5	168.1	72.2	.	.
20	IA95029-3	IABG2C1	321.6	782.5	460.7	65.5	177.2	76.0	.	.
21	IA94192-7	IABG2C0	362.5	978.2	458.8	63.9	195.9	69.6	.	.
22	IA94192-1	IABG2C0	319.4	829.8	488.4	63.5	190.8	76.5	.	.
23	IA94190-10	IABG2C0	358.0	888.7	496.6	57.4	181.7	66.9	.	.
24	IA94190-1	IABG2C0	394.1	920.7	479.3	64.3	180.5	67.1	.	.
25	IA94187-5	IABG2C0	293.6	724.1	483.5	53.0	178.2	68.6	.	.
26	IA94187-10	IABG2C0	281.5	715.4	497.8	60.9	181.5	67.9	.	.
27	IA94178-6	IABG2C0	446.6	1068.6	480.9	59.6	161.2	74.7	.	.
28	IA94178-1	IABG2C0	432.9	1030.2	469.6	58.5	162.0	69.5	.	.

Table 16. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set one evaluated in 1997 at

Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β -Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
29	IA94163-6	IABG2C0	278.6	730.3	455.1	56.5	193.9	58.8	.	.
30	IA94163-3	IABG2C0	346.1	876.1	438.4	49.7	178.6	62.1	.	.
31	IA94143-7	IABG2C0	406.1	978.5	450.9	59.2	182.6	80.5	.	.
32	IA94143-4	IABG2C0	394.1	919.8	439.5	59.0	177.8	81.6	.	.
33	IA94059-6	IABG2C0	281.4	697.1	444.4	60.2	194.4	73.9	.	.
34	IA94059-4	IABG2C0	269.0	678.3	448.3	62.0	183.6	74.7	.	.
35	IA94056-7	IABG2C0	280.3	741.3	445.7	57.8	190.6	63.0	.	.
36	IA94056-2	IABG2C0	299.2	795.8	439.2	52.6	193.8	67.9	.	.
37	IA94049-5	IABG2C0	309.2	817.3	432.6	52.3	195.2	69.9	.	.
38	IA94049-4	IABG2C0	354.2	841.8	444.2	58.5	183.9	68.0	.	.
39	IA94031-7	IABG2C0	255.9	696.8	436.7
40	IA94031-6	IABG2C0	215.4	621.9	430.4	59.3	200.2	58.2	.	.
41	IA93150-5	IABGPI	327.5	811.0	455.8	50.9	179.1	71.2	.	.
42	IA93150-1	IABGPI	309.2	743.4	454.4	59.6	192.4	64.6	.	.
43	IA93108-5	IABG1C1	377.0	912.2	460.5	53.2	166.7	63.8	.	.
44	IA93108-4	IABG1C1	338.4	841.2	450.1
45	IA93089-4	IABG1C1	474.7	1129.6	460.2	56.2	169.2	63.7	.	.
46	IA93089-1	IABG1C1	390.3	975.2	460.2	53.4	171.3	68.1	.	.
47	IA93067-5	IABGPI	305.2	756.0	497.6	52.5	170.2	82.7	.	.
48	IA93067-2	IABGPI	391.9	991.1	441.4	55.7	169.2	77.1	.	.
49	IA93061-5	IABGPI	209.9	577.5	450.2	53.4	201.3	69.0	.	.
50	IA93061-3	IABGPI	248.3	660.5	457.8	50.3	178.0	85.0	.	.
51	IA93052-6	IABG1C1	281.6	627.5	.	56.6	190.7	71.2	.	.
52	IA93052-5	IABG1C1	201.0	617.4
53	IA93034-2	IABGPI	393.8	884.4	460.7	69.1	183.5	81.6	.	.
54	IA93034-1	IABGPI	265.5	671.0	488.1
55	IA93029-6	IABG1C1	332.2	866.5	469.3	57.1	166.0	59.6	.	.
56	IA93029-4	IABG1C1	403.8	897.7	457.0	57.0	164.4	75.0	.	.

Table 16. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set one evaluated in 1997 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
57	IA93028-3	IABGPI	440.2	1053.1	453.1	49.0	174.7	80.2	.	.
58	IA93028-2	IABGPI	307.2	756.2	466.8	46.7	193.6	75.7	.	.
59	IA93014-3	IABGPI	387.5	907.3	426.0	55.6	176.2	71.3	.	.
60	IA93014-1	IABGPI	317.6	804.7	467.0	48.1	162.1	79.5	.	.
61	IA91509-4	IABG1C0	436.7	991.1	465.4	49.3	164.9	69.4	.	.
62	IA91509-2	IABG1C0	325.4	748.1	460.3	44.7	157.0	73.0	.	.
63	IA91504-2	IABG1C0	336.5	913.9	513.8	44.2	152.6	89.6	.	.
64	IA91504-11	IABG1C0	421.7	1085.5	456.4	43.3	154.6	81.4	.	.
65	IA91500-8	IABG1C0	305.8	868.3	466.3	43.4	158.0	74.5	.	.
66	IA91500-6	IABG1C0	354.0	949.8	467.9	48.4	156.0	77.8	.	.
67	IA91486-2	IABG1C0	286.0	794.9	488.3	51.6	177.3	63.5	.	.
68	IA91486-11	IABG1C0	281.7	839.9	470.3	47.0	176.2	56.6	.	.
69	IA91485-4	IABG1C0	366.1	1062.4	514.7	40.8	139.2	68.6	.	.
70	IA91485-18	IABG1C0	318.9	719.5	493.2	39.3	156.3	62.3	.	.
71	IA91479-6	IABG1C0	273.0	706.1	471.5	38.5	143.8	72.6	.	.
72	IA91479-2	IABG1C0	343.7	962.3	488.7	42.0	159.5	76.9	.	.
73	IA91478-6	IABG1C0	364.3	911.8	500.3	48.6	177.8	62.3	.	.
74	IA91478-1	IABG1C0	344.1	790.8	488.4	41.5	163.4	66.2	.	.
75	IA91470-3	IABG1C0	363.0	949.0	510.9	48.0	185.6	69.2	.	.
76	IA91470-10	IABG1C0	438.4	1040.8	472.8	54.5	177.4	60.5	.	.
77	IA91462-17	IABG1C0	397.2	991.6	494.2	47.5	161.8	75.6	.	.
78	IA91462-11	IABG1C0	286.5	758.7	487.2	53.6	186.2	73.2	.	.
79	IA91448-3	IABG1C0	327.2	883.8	482.1	48.8	190.3	72.7	.	.
80	IA91448-1	IABG1C0	324.3	836.8	487.1	51.1	186.2	71.8	.	.
81	IL82-2154	Par. line	387.1	901.3	448.1	37.8	165.2	64.6	.	.
82	D831-1-571	Par. line	380.3	910.4	454.6	57.6	176.6	72.4	.	.
83	OA926-2	Par. line	301.6	802.3	470.6	44.6	160.1	69.3	.	.
84	PI412928	Par. line	300.6	809.0	443.6	52.5	188.7	54.3	.	.

Table 16. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set one evaluated in 1997 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	PI504593	Par. line	282.0	712.9	468.6	50.7	178.6	71.3	.	.
86	Hazel	Check	333.2	792.9	483.0	52.6	166.1	85.2	.	.
87	Hazel	Check	380.1	905.7	474.1	52.6	170.6	87.6	.	.
88	Starter	Check	411.1	965.6	486.1	55.3	173.0	69.5	.	.
89	Starter	Check	325.0	823.1	498.7	56.6	182.9	66.7	.	.
90	Premier	Check	382.7	942.3	498.4	51.4	163.6	65.1	.	.
91	Premier	Check	328.2	888.1	505.7	50.8	162.9	66.6	.	.
92	Marion	Check	441.2	1027.3	442.2	54.9	156.8	74.5	.	.
93	Marion	Check	458.7	1158.4	481.7	55.0	155.7	76.2	.	.
94	Noble	Check	317.4	769.6	492.3	47.1	175.9	62.6	.	.
95	Noble	Check	282.4	730.7	508.7	47.0	188.6	60.5	.	.
96	Ogle	Check	420.1	986.5	468.3	43.8	164.2	63.0	.	.
97	Ogle	Check	437.2	979.4	460.9	39.9	149.8	67.2	.	.
98	Don	Check	337.4	756.8	463.2	43.9	156.6	75.9	.	.
99	Don	Check	381.3	869.3	462.4	48.0	153.5	74.9	.	.
100	IAN979-5-2	Check	377.7	933.8	457.1	65.6	169.7	84.3	.	.
Mean [†]			325.2	758.7	482.0	48.5	161.7	71.9		
LSD [‡]	Entry vs Entry		161.3	345.5	31.0	6.3	12.9	3.8		

[†] Mean of all entries evaluated in 1997 at Nashua.

[‡] Least significant difference at the 0.05 probability level.

Table 17. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set two evaluated in 1997 at Nashua, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
1	IA95196-7	IABG2C1	206.3	480.5	440.0	63.7	170.6	69.5	.	.
2	IA95196-5	IABG2C1	167.2	424.0	.	59.2	180.7	75.6	.	.
3	IA95189-9	IABG2C1	206.3	538.8	453.4
4	IA95189-2	IABG2C1	151.3	393.3
5	IA95181-6	IABG2C1	227.2	559.2	457.9
6	IA95181-4	IABG2C1	262.6	464.8	469.9
7	IA95172-4	IABG2C1	160.8	423.7	.	62.6	196.4	49.8	.	.
8	IA95172-1	IABG2C1	183.9	452.3	430.2
9	IA95148-3	IABG2C1	324.4	754.9	453.6	59.7	183.3	83.0	.	.
10	IA95148-1	IABG2C1	370.3	836.3	449.8	59.1	176.2	85.8	.	.
11	IA95109-3	IABG2C1	333.7	764.2	459.4	50.8	163.8	68.0	.	.
12	IA95109-2	IABG2C1	288.1	639.0	449.7	53.2	159.7	69.1	.	.
13	IA95103-6	IABG2C1	178.5	524.3	398.2	55.4	198.6	66.7	.	.
14	IA95103-3	IABG2C1	254.8	554.7	462.9	54.0	185.2	57.0	.	.
15	IA95038-9	IABG2C1	280.4	606.5	463.3	55.5	171.4	63.8	.	.
16	IA95038-7	IABG2C1	264.8	586.8	465.7	58.2	175.5	62.7	.	.
17	IA95032-9	IABG2C1	254.0	596.9	428.3	58.8	175.2	65.3	.	.
18	IA95032-6	IABG2C1	235.5	414.5	.	60.8	173.8	68.1	.	.
19	IA95029-4	IABG2C1	316.8	720.1	487.2	58.9	167.6	73.1	.	.
20	IA95029-3	IABG2C1	364.7	779.3	489.1	55.5	160.1	66.8	.	.
21	IA94192-7	IABG2C0	356.7	834.2	489.4	51.5	174.9	78.5	.	.
22	IA94192-1	IABG2C0	359.3	825.8	464.2	52.9	172.8	73.9	.	.
23	IA94190-10	IABG2C0	400.3	903.6	488.5	57.7	186.4	62.6	.	.
24	IA94190-1	IABG2C0	314.3	767.9	486.0	57.7	191.0	59.9	.	.
25	IA94187-5	IABG2C0	311.0	679.0	470.7	61.2	168.1	79.9	.	.
26	IA94187-10	IABG2C0	366.9	886.9	462.8	56.0	187.7	75.8	.	.
27	IA94178-6	IABG2C0	243.3	614.9	472.4	56.0	192.0	49.2	.	.
28	IA94178-1	IABG2C0	247.4	576.6	460.3	57.5	192.2	53.6	.	.

Table 17. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set two evaluated in 1997 at

Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
29	IA94163-6	IABG2C0	267.9	679.9	469.7	54.2	197.4	71.0	.	.
30	IA94163-3	IABG2C0	395.2	817.6	450.0	54.8	167.6	78.7	.	.
31	IA94143-7	IABG2C0	188.1	695.6	339.8	60.3	196.5	63.5	.	.
32	IA94143-4	IABG2C0	266.5	629.4	455.1	60.8	175.2	70.2	.	.
33	IA94059-6	IABG2C0	313.1	713.8	487.2	64.1	170.8	75.9	.	.
34	IA94059-4	IABG2C0	350.1	797.0	499.5	56.5	168.3	68.3	.	.
35	IA94056-7	IABG2C0	296.1	721.8	444.7	55.5	184.3	62.3	.	.
36	IA94056-2	IABG2C0	215.9	722.6	451.9	55.4	193.9	62.8	.	.
37	IA94049-5	IABG2C0	348.3	792.7	493.1	47.3	166.5	75.6	.	.
38	IA94049-4	IABG2C0	291.2	731.4	505.3	52.0	170.2	62.7	.	.
39	IA94031-7	IABG2C0	193.8	519.3	437.3	58.7	204.2	64.9	.	.
40	IA94031-6	IABG2C0	203.2	501.7	420.6	56.2	193.4	65.5	.	.
41	IA93150-5	IABG1C1	389.2	912.2	480.6	58.7	179.6	62.6	.	.
42	IA93150-1	IABG1C1	417.6	897.0	498.6	56.5	180.9	63.4	.	.
43	IA93108-5	IABG1C1	412.9	857.6	492.9	51.0	178.9	63.4	.	.
44	IA93108-4	IABG1C1	390.7	854.5	479.6	57.9	179.3	58.7	.	.
45	IA93089-4	IABG1C1	442.4	875.6	469.1	52.8	171.3	70.3	.	.
46	IA93089-1	IABG1C1	297.6	698.8	471.1	48.8	163.9	62.4	.	.
47	IA93067-5	IABG1C1	311.7	768.7	487.1	56.0	179.9	68.3	.	.
48	IA93067-2	IABG1C1	364.2	875.1	480.3	58.2	175.1	75.8	.	.
49	IA93061-5	IABG1C1	382.3	846.3	461.6	50.3	165.9	64.1	.	.
50	IA93061-3	IABG1C1	376.8	807.4	464.3	53.0	177.6	65.6	.	.
51	IA93052-6	IABG1C1	245.3	710.3	484.9	56.3	173.9	74.3	.	.
52	IA93052-5	IABG1C1	291.5	703.2	474.8	56.3	190.2	77.5	.	.
53	IA93034-2	IABG1C1	443.7	983.3	471.0	55.6	182.2	75.0	.	.
54	IA93034-1	IABG1C1	418.3	914.8	487.1	51.0	176.8	72.6	.	.
55	IA93029-6	IABG1C1	237.5	661.0	455.8	55.0	216.7	57.2	.	.
56	IA93029-4	IABG1C1	297.7	693.6	427.2	51.5	198.8	61.8	.	.

Table 17. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set two evaluated in 1997 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
57	IA93028-3	IABG1C1	389.0	878.4	492.2	47.0	153.9	73.8	.	.
58	IA93028-2	IABG1C1	414.5	868.9	457.5	50.3	159.2	70.2	.	.
59	IA93014-3	IABG1C1	389.8	815.6	488.6	47.5	154.0	76.7	.	.
60	IA93014-1	IABG1C1	403.5	833.9	475.4	51.2	169.6	68.0	.	.
61	IA91509-4	IABG1C0	321.7	816.9	496.6	42.8	151.2	67.7	.	.
62	IA91509-2	IABG1C0	262.8	705.8	449.2	48.3	178.7	74.5	.	.
63	IA91504-2	IABG1C0	271.2	745.4	469.4	39.1	163.9	70.7	.	.
64	IA91504-11	IABG1C0	279.6	772.5	448.8
65	IA91500-8	IABG1C0	238.2	773.7	418.4	51.9	184.7	80.7	.	.
66	IA91500-6	IABG1C0	276.5	814.7	458.1	50.9	172.9	82.7	.	.
67	IA91486-2	IABG1C0	93.5	338.5
68	IA91486-11	IABG1C0	125.6	330.0
69	IA91485-4	IABG1C0	307.3	810.9	452.6	50.3	168.2	68.8	.	.
70	IA91485-18	IABG1C0	296.2	776.7	494.1	51.8	175.0	64.6	.	.
71	IA91479-6	IABG1C0	276.7	665.1	469.0	39.2	149.6	73.9	.	.
72	IA91479-2	IABG1C0	249.7	605.9	442.9	39.4	144.2	77.0	.	.
73	IA91478-6	IABG1C0	291.4	621.2	478.2	51.0	181.7	79.2	.	.
74	IA91478-1	IABG1C0	382.3	910.3	472.4	51.5	147.3	74.2	.	.
75	IA91470-3	IABG1C0	377.3	891.7	472.1	50.3	181.6	74.6	.	.
76	IA91470-10	IABG1C0	371.8	965.3	477.0	50.2	173.7	68.2	.	.
77	IA91462-17	IABG1C0	396.4	859.3	452.6	51.8	177.1	72.7	.	.
78	IA91462-11	IABG1C0	381.7	874.9	472.8	51.5	185.6	65.7	.	.
79	IA91448-3	IABG1C0	295.2	746.2	443.5	51.1	174.1	69.3	.	.
80	IA91448-1	IABG1C0	417.2	951.1	473.7	48.7	168.5	76.3	.	.
81	H52-5	Par. line	365.4	809.1	458.6	45.9	153.1	82.9	.	.
82	P7869D1-5 [†]	Par. line	198.1	668.8	488.1	45.7	172.9	64.5	.	.
83	NO5-1	Par. line	204.4	524.7	.	36.2	165.2	65.0	.	.
84	CO5406..380	Par. line	266.8	410.7

Table 17. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set two evaluated in 1997 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	PI504601	Par. line	226.4	506.2	497.1	52.8	183.0	77.0	.	.
86	Hazel	Check	362.1	786.7	479.3	50.4	162.9	88.7	.	.
87	Hazel	Check	365.8	794.3	481.8	46.5	163.5	88.2	.	.
88	Starter	Check	363.8	807.7	495.4	50.4	167.4	69.9	.	.
89	Starter	Check	303.6	685.7	494.8	54.8	178.2	65.2	.	.
90	Premier	Check	368.3	804.8	516.9	49.5	155.8	66.0	.	.
91	Premier	Check	310.4	687.5	496.7	52.4	159.8	64.5	.	.
92	Marion	Check	407.6	948.3	463.6	50.8	149.3	77.6	.	.
93	Marion	Check	322.0	818.1	456.1	53.3	159.4	77.0	.	.
94	Noble	Check	279.9	733.9	497.6	44.5	172.8	60.4	.	.
95	Noble	Check	301.2	716.7	495.4	40.5	170.5	64.7	.	.
96	Ogle	Check	393.3	869.6	457.8	37.1	149.6	65.2	.	.
97	Ogle	Check	442.7	944.3	461.8	40.0	151.3	66.6	.	.
98	Don	Check	386.8	838.2	469.3	42.9	152.9	75.1	.	.
99	Don	Check	249.1	674.2	488.1	47.4	154.3	74.5	.	.
100	IAN979-5-2	Check	389.2	869.3	465.1	63.8	165.5	86.4	.	.
Mean [†]			325.2	758.7	482.0	48.5	161.7	71.9		
LSD [‡]	Entry vs Entry		161.3	345.5	31.0	6.3	12.9	3.8		

[†] Mean of all entries evaluated in 1997 at Nashua.

[‡] Least significant difference at the 0.05 probability level.

Table 18. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set three evaluated in 1997 at

Nashua, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
1	IA95196-7	IABG2C1	310.8	426.2	451.4					
2	IA95196-5	IABG2C1	205.5	447.7	440.4	55.8	164.7	68.9		
3	IA95189-9	IABG2C1	346.7	838.5	464.4	54.6	178.9	83.2		
4	IA95189-2	IABG2C1	286.6	651.7	496.1	57.4	195.3	70.3		
5	IA95181-6	IABG2C1	360.3	851.7	475.6	59.8	190.9	74.9		
6	IA95181-4	IABG2C1	313.1	715.3	459.6	61.0	196.8	67.4		
7	IA95172-4	IABG2C1	224.7	564.4		61.1	188.9	51.6		
8	IA95172-1	IABG2C1	234.1	561.0	447.6	63.8	186.2	56.8		
9	IA95148-3	IABG2C1	195.5	524.4		57.7	180.4	70.5		
10	IA95148-1	IABG2C1	288.3	650.2	488.8	58.6	169.0	66.0		
11	IA95109-3	IABG2C1	221.2	508.4	428.3	65.8	174.1	73.3		
12	IA95109-2	IABG2C1	240.0	566.7	463.9	66.2	170.4	73.8		
13	IA95103-6	IABG2C1	276.7	633.1	462.4	56.4	180.2	62.5		
14	IA95103-3	IABG2C1	265.8	655.4	461.6	58.0	179.1	65.0		
15	IA95038-9	IABG2C1	294.8	678.1	460.7	60.1	168.8	65.8		
16	IA95038-7	IABG2C1	273.8	644.0	448.8	60.0	171.9	66.8		
17	IA95032-9	IABG2C1	213.8	547.3	394.6	55.4	191.5	58.8		
18	IA95032-6	IABG2C1	243.9	577.8	460.6	52.6	184.6	63.9		
19	IA95029-4	IABG2C1	245.6	647.1		65.1	178.4	68.8		
20	IA95029-3	IABG2C1	284.0	678.9	468.1					
21	IA94192-7	IABG2C0	320.6	751.2	468.3	58.4	192.1	69.2		
22	IA94192-1	IABG2C0	285.0	664.6	454.7	57.5	185.9	73.9		
23	IA94190-10	IABG2C0	266.4	648.6	454.1	57.7	174.7	57.2		
24	IA94190-1	IABG2C0	313.0	696.3	443.2	54.6	174.8	58.3		
25	IA94187-5	IABG2C0	379.2	761.7	488.9	56.9	184.2	75.0		
26	IA94187-10	IABG2C0	395.4	926.3	484.5	55.3	180.7	79.8		
27	IA94178-6	IABG2C0	275.6	684.0	459.1	61.2	185.8	54.1		
28	IA94178-1	IABG2C0	308.8	682.0	471.6	58.7	178.1	55.3		

Table 18. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set three evaluated in 1997 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
29	IA94163-6	IABG2C0	168.5	484.1
30	IA94163-3	IABG2C0	292.8	696.7	482.6	62.2	189.6	57.1	.	.
31	IA94143-7	IABG2C0	352.4	791.8	441.8	52.5	174.8	63.5	.	.
32	IA94143-4	IABG2C0	273.7	736.3	477.4	52.8	188.3	66.4	.	.
33	IA94059-6	IABG2C0	230.3	591.9	404.5	55.7	185.0	67.2	.	.
34	IA94059-4	IABG2C0	244.4	582.4	420.7	58.4	181.5	70.8	.	.
35	IA94056-7	IABG2C0	278.9	687.9	441.9	56.8	181.1	58.8	.	.
36	IA94056-2	IABG2C0	334.6	757.7	481.5	52.9	165.9	68.1	.	.
37	IA94049-5	IABG2C0	305.6	699.3	461.2	57.4	174.5	67.0	.	.
38	IA94049-4	IABG2C0	309.7	691.2	430.9	60.2	172.5	63.1	.	.
39	IA94031-7	IABG2C0	443.3	921.8	480.3	52.9	166.6	65.8	.	.
40	IA94031-6	IABG2C0	423.8	883.6	474.2	63.1	169.5	70.6	.	.
41	IA93150-5	IABG1C1	293.1	873.1	472.4	52.1	182.7	70.2	.	.
42	IA93150-1	IABG1C1	394.9	915.8	493.9	63.3	180.1	69.0	.	.
43	IA93108-5	IABGPI	349.8	802.0	424.1	54.8	181.6	74.5	.	.
44	IA93108-4	IABGPI	327.2	854.6	433.4	54.4	178.9	78.6	.	.
45	IA93089-4	IABGPI	285.0	680.9	439.8	55.1	170.4	74.3	.	.
46	IA93089-1	IABGPI	343.0	808.5	449.0	49.3	166.9	71.3	.	.
47	IA93067-5	IABG1C1	405.1	917.5	455.2	48.1	174.0	66.0	.	.
48	IA93067-2	IABG1C1	352.5	774.7	454.5	56.1	181.2	60.0	.	.
49	IA93061-5	IABG1C1	346.9	785.5	478.6	54.2	182.9	77.4	.	.
50	IA93061-3	IABG1C1	335.8	757.5	488.9	52.9	179.0	75.1	.	.
51	IA93052-6	IABG1C1	280.4	695.6	465.1	62.5	174.0	76.6	.	.
52	IA93052-5	IABG1C1	360.0	800.6	473.2	55.9	160.1	74.9	.	.
53	IA93034-2	IABG1C1	387.2	892.8	469.9	66.6	174.3	72.4	.	.
54	IA93034-1	IABG1C1	345.5	816.5	488.7	59.6	181.8	71.7	.	.
55	IA93029-6	IABGPI	400.7	950.5	460.8	55.6	176.2	75.1	.	.
56	IA93029-4	IABGPI	313.4	796.2	400.6	50.4	164.8	72.1	.	.

Table 18. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set three evaluated in 1997 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
57	IA93028-3	IABGPI	354.2	877.7	461.8	49.7	175.6	76.9	.	.
58	IA93028-2	IABGPI	290.8	739.0	447.3
59	IA93014-3	IABG1C1	403.8	908.5	446.2	49.6	149.7	75.4	.	.
60	IA93014-1	IABG1C1	348.6	760.0	469.6	48.9	148.6	73.1	.	.
61	IA91509-4	IABG1C0	300.5	682.7	455.8	55.5	166.1	78.5	.	.
62	IA91509-2	IABG1C0	419.8	931.8	452.1	50.7	171.2	86.0	.	.
63	IA91504-2	IABG1C0	257.8	560.2	.	50.9	182.3	70.2	.	.
64	IA91504-11	IABG1C0	307.9	735.1	493.7	41.2	148.1	69.0	.	.
65	IA91500-8	IABG1C0	284.1	616.8	474.7	48.3	165.6	75.2	.	.
66	IA91500-6	IABG1C0	293.9	751.8	492.7	50.3	172.7	62.9	.	.
67	IA91486-2	IABG1C0	294.5	660.0	472.0	48.8	163.2	70.1	.	.
68	IA91486-11	IABG1C0	287.1	727.6	511.7	43.9	171.2	77.9	.	.
69	IA91485-4	IABG1C0	306.5	738.4	476.4	50.8	163.2	77.6	.	.
70	IA91485-18	IABG1C0	308.0	750.7	463.1	39.4	157.3	82.9	.	.
71	IA91479-6	IABG1C0	278.3	729.6	453.0	52.2	177.4	68.7	.	.
72	IA91479-2	IABG1C0	269.2	642.9	493.0	46.9	161.0	71.1	.	.
73	IA91478-6	IABG1C0	404.3	917.0	483.8	59.6	166.2	81.8	.	.
74	IA91478-1	IABG1C0	267.2	624.6	486.9	51.2	171.3	73.1	.	.
75	IA91470-3	IABG1C0	387.9	863.0	472.4	54.0	181.3	74.0	.	.
76	IA91470-10	IABG1C0	344.4	777.2	458.9	42.5	157.4	68.3	.	.
77	IA91462-17	IABG1C0	354.6	850.8	458.7	62.6	177.0	82.8	.	.
78	IA91462-11	IABG1C0	343.8	734.0	458.6	50.8	171.5	78.7	.	.
79	IA91448-3	IABG1C0	417.2	976.1	481.6	47.9	158.4	62.4	.	.
80	IA91448-1	IABG1C0	403.9	913.5	461.1	44.7	154.4	67.8	.	.
81	H87-7-4	Par. line	413.8	924.3	474.9	44.6	152.6	72.4	.	.
82	MO07929	Par. line	409.5	912.8	450.9	55.1	173.8	87.0	.	.
83	MN88156	Par. line	249.2	597.9	451.5	54.3	205.0	52.9	.	.
84	NO4-8	Par. line	320.2	743.3

Table 18. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set three evaluated in 1997 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	PI361884	Par. line	352.7	800.6	506.5	44.2	151.8	72.1	.	.
86	Hazel	Check	364.5	793.2	481.2	47.3	161.1	87.0	.	.
87	Hazel	Check	325.4	733.4	479.2	52.2	167.9	86.0	.	.
88	Starter	Check	348.5	814.8	478.4	51.0	172.9	68.7	.	.
89	Starter	Check	313.2	715.0	486.6	53.0	173.7	67.3	.	.
90	Premier	Check	323.5	741.9	521.1	50.5	157.1	66.3	.	.
91	Premier	Check	361.8	791.0	501.4	53.7	154.0	66.4	.	.
92	Marion	Check	374.3	954.4	457.2	53.9	160.9	74.8	.	.
93	Marion	Check	515.9	1192.9	470.0	50.0	159.0	75.2	.	.
94	Noble	Check	311.1	700.2	503.7	42.6	170.3	64.6	.	.
95	Noble	Check	311.7	711.9	501.7	42.4	179.8	64.8	.	.
96	Ogle	Check	407.6	886.1	445.6	38.5	154.4	67.1	.	.
97	Ogle	Check	332.6	742.1	450.4	37.8	150.1	67.7	.	.
98	Don	Check	324.2	731.5	485.3	45.9	159.7	76.4	.	.
99	Don	Check	324.1	714.7	478.6	50.0	153.0	74.5	.	.
100	IAN979-5-2	Check	365.0	833.6	458.3	62.6	166.5	83.5	.	.
Mean [†]			325.2	758.7	482.0	48.5	161.7	71.9		
LSD [‡]	Entry vs Entry		161.3	345.5	31.0	6.3	12.9	3.8		

[†] Mean of all entries evaluated in 1997 at Nashua.

[‡] Least significant difference at the 0.05 probability level.

Table 19. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set four evaluated in 1997 at

Nashua, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
1	IA95196-7	IABG2C1	202.3	449.6
2	IA95196-5	IABG2C1	266.5	618.1	433.0	54.5	187.5	63.1	.	.
3	IA95189-9	IABG2C1	163.5	355.2
4	IA95189-2	IABG2C1	204.4	487.4	430.9	59.6	199.6	69.6	.	.
5	IA95181-6	IABG2C1	239.9	620.0	462.5	65.2	199.7	68.1	.	.
6	IA95181-4	IABG2C1	204.4	523.3	428.0	61.0	207.9	56.5	.	.
7	IA95172-4	IABG2C1	225.6	615.8
8	IA95172-1	IABG2C1	342.0	794.5	426.2	61.3	186.0	77.4	.	.
9	IA95148-3	IABG2C1	263.8	622.1	493.6	62.1	189.8	71.7	.	.
10	IA95148-1	IABG2C1	300.8	695.7	460.7	62.5	181.5	79.3	.	.
11	IA95109-3	IABG2C1	180.0	450.3
12	IA95109-2	IABG2C1	327.9	335.7	.	50.0	175.3	69.5	.	.
13	IA95103-6	IABG2C1	294.8	640.3	473.1	54.7	173.2	72.1	.	.
14	IA95103-3	IABG2C1	291.3	659.4	478.5	52.8	172.7	75.1	.	.
15	IA95038-9	IABG2C1	267.1	646.3	452.3	56.0	186.0	64.9	.	.
16	IA95038-7	IABG2C1	139.2	313.5	.	58.5	190.2	68.5	.	.
17	IA95032-9	IABG2C1	219.4	497.4	440.9	61.2	188.2	65.5	.	.
18	IA95032-6	IABG2C1	265.6	559.4	464.8	64.0	179.5	73.3	.	.
19	IA95029-4	IABG2C1	236.7	650.9	439.9	62.2	205.2	62.4	.	.
20	IA95029-3	IABG2C1	219.9	570.2	424.1	63.1	198.2	56.2	.	.
21	IA94192-7	IABG2C0	323.7	665.6	468.7	65.4	188.0	71.7	.	.
22	IA94192-1	IABG2C0	394.0	825.9	467.3	67.6	184.2	73.7	.	.
23	IA94190-10	IABG2C0	342.9	815.6	496.3	55.3	180.4	66.7	.	.
24	IA94190-1	IABG2C0	275.3	702.8	473.9	54.1	179.9	59.4	.	.
25	IA94187-5	IABG2C0	323.1	748.5	450.8	59.3	185.0	78.8	.	.
26	IA94187-10	IABG2C0	393.1	864.7	472.7	58.2	175.4	80.1	.	.
27	IA94178-6	IABG2C0	323.4	744.7	462.1	63.2	172.4	74.8	.	.
28	IA94178-1	IABG2C0	352.7	761.8	479.8	57.4	181.5	82.5	.	.

Table 19. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set four evaluated in 1997 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
29	IA94163-6	IABG2C0	421.8	871.6	466.5	53.2	169.9	73.9	.	.
30	IA94163-3	IABG2C0	417.3	936.3	484.3	52.8	177.0	71.5	.	.
31	IA94143-7	IABG2C0	249.2	674.9	392.1	63.6	204.7	49.1	.	.
32	IA94143-4	IABG2C0	292.1	683.4	433.0
33	IA94059-6	IABG2C0	374.2	844.3	424.8	56.0	180.5	72.7	.	.
34	IA94059-4	IABG2C0	230.7	439.5	.	54.8	206.4	64.2	.	.
35	IA94056-7	IABG2C0	255.8	631.6	433.5	60.9	204.5	58.6	.	.
36	IA94056-2	IABG2C0	308.6	708.5	426.5	57.5	189.7	64.7	.	.
37	IA94049-5	IABG2C0	226.4	633.7	498.9	49.4	200.4	69.0	.	.
38	IA94049-4	IABG2C0	299.6	735.8	492.1	52.8	194.8	68.2	.	.
39	IA94031-7	IABG2C0	277.0	693.2	492.5	58.0	175.3	63.5	.	.
40	IA94031-6	IABG2C0	315.0	764.3	460.3	50.6	177.6	66.8	.	.
41	IA93150-5	IABGPI	382.9	848.6	436.1	47.8	164.1	84.7	.	.
42	IA93150-1	IABGPI	259.7	653.8	394.8	50.4	171.1	77.3	.	.
43	IA93108-5	IABG1C1	401.1	922.5	505.8	50.8	180.5	78.9	.	.
44	IA93108-4	IABG1C1	416.9	1002.2	470.6	57.3	195.0	82.3	.	.
45	IA93089-4	IABG1C1	403.3	897.1	496.7
46	IA93089-1	IABG1C1	458.8	1071.9	456.4	51.4	185.2	70.9	.	.
47	IA93067-5	IABGPI	315.1	672.6	459.9	55.1	174.8	76.1	.	.
48	IA93067-2	IABGPI	382.7	824.2	474.3
49	IA93061-5	IABGPI	242.7	607.3	347.6	53.2	171.4	74.8	.	.
50	IA93061-3	IABGPI	444.4	980.2	443.8	50.2	181.8	77.6	.	.
51	IA93052-6	IABG1C1	393.6	880.4	465.6	59.1	164.1	69.7	.	.
52	IA93052-5	IABG1C1	398.9	887.1	496.1	58.1	181.4	63.6	.	.
53	IA93034-2	IABG1C1	381.8	839.7	460.2	62.4	186.0	68.4	.	.
54	IA93034-1	IABG1C1	343.1	789.0	463.2	60.3	189.8	68.8	.	.
55	IA93029-6	IABG1C1	440.1	997.4	482.6	55.7	172.3	71.3	.	.
56	IA93029-4	IABG1C1	387.1	914.2	493.6	54.7	174.1	74.7	.	.

Table 19. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set four evaluated in 1997 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
57	IA93028-3	IABGPI	155.4	371.5
58	IA93028-2	IABGPI	191.9	522.0	454.1	56.1	191.6	67.3	.	.
59	IA93014-3	IABG1C1	419.8	930.1	427.6	52.7	177.3	70.6	.	.
60	IA93014-1	IABG1C1	371.0	755.3	452.8	54.7	175.4	64.7	.	.
61	IA91509-4	IABG1C0	383.2	839.6	470.4	48.9	166.3	71.3	.	.
62	IA91509-2	IABG1C0	387.0	899.2	457.8	52.7	185.5	74.0	.	.
63	IA91504-2	IABG1C0	307.2	688.0	493.4	44.5	159.5	69.6	.	.
64	IA91504-11	IABG1C0	299.5	658.6	496.9	34.8	146.3	73.0	.	.
65	IA91500-8	IABG1C0	376.5	908.0	443.7	40.3	153.8	80.0	.	.
66	IA91500-6	IABG1C0	373.2	915.3	475.2	42.6	159.3	70.7	.	.
67	IA91486-2	IABG1C0	399.0	945.0	474.8	42.4	142.1	73.9	.	.
68	IA91486-11	IABG1C0	411.9	953.9	490.5	43.1	136.7	66.2	.	.
69	IA91485-4	IABG1C0	300.7	671.2	459.9	45.8	147.6	62.3	.	.
70	IA91485-18	IABG1C0	190.4	421.6	.	39.6	151.3	69.2	.	.
71	IA91479-6	IABG1C0	456.6	1011.6	477.8	52.8	163.3	67.0	.	.
72	IA91479-2	IABG1C0	422.4	906.3	463.5	46.2	156.2	78.6	.	.
73	IA91478-6	IABG1C0	369.5	799.8	463.9	53.4	168.5	73.2	.	.
74	IA91478-1	IABG1C0	442.3	909.3	472.9	46.0	159.9	70.8	.	.
75	IA91470-3	IABG1C0	393.8	941.1	460.3	46.1	168.0	64.3	.	.
76	IA91470-10	IABG1C0	467.4	1023.0	460.3	53.0	184.7	60.9	.	.
77	IA91462-17	IABG1C0	343.5	802.8	477.9	52.5	178.2	63.0	.	.
78	IA91462-11	IABG1C0	419.4	921.9	486.8
79	IA91448-3	IABG1C0	398.5	863.4	472.4	53.4	178.1	60.8	.	.
80	IA91448-1	IABG1C0	453.5	972.7	450.6	51.8	160.5	77.1	.	.
81	H730-12	Par. line	362.3	764.3	452.9	45.8	162.0	80.3	.	.
82	MN86226	Par. line	306.4	709.0	508.7	53.4	184.2	63.5	.	.
83	NO20-1	Par. line	145.2	271.5	.	46.4	166.3	73.5	.	.
84	PI361886	Par. line	227.9	552.6

Table 19. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set four evaluated in 1997 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	PI502955	Par. line	309.3	762.6	432.5	62.3	185.4	72.3	.	.
86	Hazel	Check	349.5	778.8	472.4	49.9	156.7	92.1	.	.
87	Hazel	Check	346.3	758.6	495.9	48.0	165.4	90.8	.	.
88	Starter	Check	360.4	874.5	496.9	55.3	170.5	68.9	.	.
89	Starter	Check	282.5	670.8	483.2	51.6	171.0	68.0	.	.
90	Premier	Check	378.5	836.0	509.1	51.3	155.2	66.0	.	.
91	Premier	Check	403.7	892.5	518.6	50.8	154.0	65.7	.	.
92	Marion	Check	449.7	1023.4	471.9	55.0	153.9	74.7	.	.
93	Marion	Check	430.9	1030.0	433.6	52.9	155.1	75.0	.	.
94	Noble	Check	347.7	778.2	479.6
95	Noble	Check	333.9	810.2	484.9	45.7	181.0	61.1	.	.
96	Ogle	Check	398.5	829.6	460.4	41.7	150.1	64.5	.	.
97	Ogle	Check	294.8	606.1	460.4	47.1	163.3	67.3	.	.
98	Don	Check	336.2	774.1	469.1	45.7	152.9	73.4	.	.
99	Don	Check	288.6	622.9	453.6	45.7	156.2	74.9	.	.
100	IAN979-5-2	Check	395.9	913.8	462.7
Mean [†]			325.2	758.7	482.0	48.5	161.7	71.9		
LSD [‡]	Entry vs Entry		161.3	345.5	31.0	6.3	12.9	3.8		

[†] Mean of all entries evaluated in 1997 at Nashua.

[‡] Least significant difference at the 0.05 probability level.

Table 20. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set five evaluated in 1997 at

Nashua, IA.

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
1	IA95196-7	IABG2C1	397.8	842.7	466.1	64.3	179.6	77.7	.	.
2	IA95196-5	IABG2C1	260.8	598.4	501.1	66.0	185.4	70.6	.	.
3	IA95189-9	IABG2C1	253.2	594.0	476.4	52.1	169.5	70.0	.	.
4	IA95189-2	IABG2C1	304.0	716.0	486.9	51.1	170.2	64.8	.	.
5	IA95181-6	IABG2C1	318.0	754.5	470.2	57.4	173.2	65.9	.	.
6	IA95181-4	IABG2C1	306.6	726.5	484.4	58.7	168.1	72.3	.	.
7	IA95172-4	IABG2C1	172.4	415.5
8	IA95172-1	IABG2C1	212.1	514.2	435.8	64.2	182.4	57.5	.	.
9	IA95148-3	IABG2C1	344.5	740.7	465.1	60.1	164.7	76.0	.	.
10	IA95148-1	IABG2C1	387.6	801.0	456.3	55.4	158.2	69.6	.	.
11	IA95109-3	IABG2C1	201.4	447.0	.	57.8	179.6	69.9	.	.
12	IA95109-2	IABG2C1	245.8	614.2	471.4	58.9	180.7	71.9	.	.
13	IA95103-6	IABG2C1	236.6	555.7	442.1	62.6	180.7	64.5	.	.
14	IA95103-3	IABG2C1	188.0	504.0	375.6	63.2	192.1	63.5	.	.
15	IA95038-9	IABG2C1	346.3	719.7	460.4	62.7	171.0	82.2	.	.
16	IA95038-7	IABG2C1	339.6	730.6	470.0	66.0	179.4	84.6	.	.
17	IA95032-9	IABG2C1	351.4	772.8	481.6	65.5	173.3	74.6	.	.
18	IA95032-6	IABG2C1	293.2	699.6	482.1	67.2	169.7	74.7	.	.
19	IA95029-4	IABG2C1	152.5	325.0	.	58.0	169.2	62.0	.	.
20	IA95029-3	IABG2C1	138.7	332.3	.	58.8	182.0	61.9	.	.
21	IA94192-7	IABG2C0	342.6	781.0	479.6	61.4	176.5	62.4	.	.
22	IA94192-1	IABG2C0	316.2	733.4	483.4	63.9	164.7	73.6	.	.
23	IA94190-10	IABG2C0	266.1	667.4	448.4	57.7	190.4	78.3	.	.
24	IA94190-1	IABG2C0	349.2	776.8	461.1	59.7	185.3	80.3	.	.
25	IA94187-5	IABG2C0	262.2	736.5	476.6	56.2	180.8	62.4	.	.
26	IA94187-10	IABG2C0	300.3	737.6	467.3	56.4	166.2	68.2	.	.
27	IA94178-6	IABG2C0	351.4	784.4	488.8	58.2	194.8	63.0	.	.
28	IA94178-1	IABG2C0	329.6	785.4	478.1	58.2	186.3	63.5	.	.

Table 20. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set five evaluated in 1997 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
29	IA94163-6	IABG2C0	339.2	790.5	493.5	60.3	182.9	70.0	.	.
30	IA94163-3	IABG2C0	406.9	882.7	482.6	66.6	176.9	74.7	.	.
31	IA94143-7	IABG2C0	384.1	851.8	507.1	53.1	173.6	68.0	.	.
32	IA94143-4	IABG2C0	387.7	847.2	508.1	51.6	174.9	67.8	.	.
33	IA94059-6	IABG2C0	286.5	692.0	472.3	58.8	189.9	61.3	.	.
34	IA94059-4	IABG2C0	345.5	742.2	476.6	57.9	189.9	55.1	.	.
35	IA94056-7	IABG2C0	374.6	799.9	464.0	52.4	179.6	68.1	.	.
36	IA94056-2	IABG2C0	404.4	857.7	463.1	59.2	160.5	76.6	.	.
37	IA94049-5	IABG2C0	455.1	936.5	478.6	54.2	167.7	67.5	.	.
38	IA94049-4	IABG2C0	419.6	816.3	454.2	47.0	150.3	67.7	.	.
39	IA94031-7	IABG2C0	305.7	647.2	473.1	54.5	166.1	67.6	.	.
40	IA94031-6	IABG2C0	394.7	807.9	458.9	56.2	162.5	64.2	.	.
41	IA93150-5	IABG1C1	407.9	885.1	438.9	60.4	176.0	66.3	.	.
42	IA93150-1	IABG1C1	387.3	838.4	457.7	53.8	162.5	71.3	.	.
43	IA93108-5	IABG1C1	325.6	812.6	484.1	57.7	178.2	69.9	.	.
44	IA93108-4	IABG1C1	374.6	852.8	449.1	52.8	185.6	65.0	.	.
45	IA93089-4	IABG1C1	357.1	587.5	.	54.6	195.5	69.2	.	.
46	IA93089-1	IABG1C1	278.4	594.2	484.0	52.0	191.9	62.8	.	.
47	IA93067-5	IABG1C1	289.6	636.9	480.6	48.7	191.5	73.7	.	.
48	IA93067-2	IABG1C1	359.4	788.7	482.9	53.0	188.6	71.4	.	.
49	IA93061-5	IABG1C1	425.6	975.5	482.6	50.8	178.1	69.8	.	.
50	IA93061-3	IABG1C1	425.1	949.2	479.6	54.6	181.4	72.2	.	.
51	IA93052-6	IABG1C1	248.3	669.2	416.1	60.4	200.6	69.9	.	.
52	IA93052-5	IABG1C1	239.9	585.1	440.7	58.8	201.1	69.8	.	.
53	IA93034-2	IABGPI	411.8	816.5	426.6	52.9	177.0	84.7	.	.
54	IA93034-1	IABGPI	355.7	769.8	431.5	55.9	190.5	78.6	.	.
55	IA93029-6	IABGPI	198.4	580.7
56	IA93029-4	IABGPI	315.6	776.4	430.3	49.9	181.9	65.1	.	.

Table 20. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set five evaluated in 1997 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
57	IA93028-3	IABG1C1	426.6	903.6	480.2	49.2	155.8	74.5	.	.
58	IA93028-2	IABG1C1	311.3	724.8	486.2	53.4	160.3	79.6	.	.
59	IA93014-3	IABGPI	313.5	731.5	450.9	46.0	168.1	79.0	.	.
60	IA93014-1	IABGPI	389.0	900.6	475.0	46.9	168.8	80.3	.	.
61	IA91509-4	IABG1C0	394.8	655.1	428.2	44.8	158.0	69.6	.	.
62	IA91509-2	IABG1C0	396.2	809.8	460.8	48.1	150.6	63.1	.	.
63	IA91504-2	IABG1C0	234.9	568.1	471.6	40.2	144.9	83.4	.	.
64	IA91504-11	IABG1C0	232.7	631.5	436.6	46.7	176.6	78.3	.	.
65	IA91500-8	IABG1C0	323.3	795.2	454.0	50.0	165.2	77.6	.	.
66	IA91500-6	IABG1C0	250.6	604.6	459.9	47.8	162.9	75.7	.	.
67	IA91486-2	IABG1C0	417.7	920.7	455.3	51.2	156.8	70.1	.	.
68	IA91486-11	IABG1C0	395.6	869.1	464.8	57.3	175.9	68.1	.	.
69	IA91485-4	IABG1C0	368.1	826.1	470.7	44.0	171.6	61.9	.	.
70	IA91485-18	IABG1C0	371.7	812.6	489.2	51.9	168.2	69.1	.	.
71	IA91479-6	IABG1C0	426.4	896.1	479.3	54.3	168.2	75.2	.	.
72	IA91479-2	IABG1C0	373.9	824.8	467.3	48.6	164.3	71.9	.	.
73	IA91478-6	IABG1C0	374.7	786.8	473.9	46.9	168.6	71.9	.	.
74	IA91478-1	IABG1C0	335.8	752.8	486.2	47.7	179.3	67.6	.	.
75	IA91470-3	IABG1C0	338.5	713.1	502.7	46.2	177.0	67.9	.	.
76	IA91470-10	IABG1C0	324.9	879.2	452.3	52.7	206.5	70.3	.	.
77	IA91462-17	IABG1C0	404.1	1044.4	435.6	48.3	185.5	67.9	.	.
78	IA91462-11	IABG1C0	436.0	845.7	488.4	47.8	149.6	73.0	.	.
79	IA91448-3	IABG1C0	391.2	859.9	494.8	54.0	157.8	76.5	.	.
80	IA91448-1	IABG1C0	368.6	786.6	505.9	56.0	168.8	74.9	.	.
81	H688-11	Par. line	399.3	871.8	468.2	48.4	156.1	79.3	.	.
82	IL85-6183-1	Par. line	328.2	698.4	456.0	54.0	177.4	69.1	.	.
83	D921-255	Par. line	279.7	614.0	431.4	51.2	151.9	79.4	.	.
84	NO10-1	Par. line	172.2	308.2

Table 20. Mean agronomic and grain quality traits of experimental oat lines and check cultivars from set five evaluated in 1997 at Nashua, IA (continued).

Entry	Line	Population	Grain yield g m ⁻²	Biomass g m ⁻²	Test weight kg m ⁻³	β-Glucan content g kg ⁻¹	Protein content g kg ⁻¹	Oil content g kg ⁻¹	Heading date dap	Height cm
85	NO11-1	Par. line	98.7	290.2	.	58.4	212.5	69.8	.	.
86	Hazel	Check	357.5	843.0	499.5	49.1	163.1	90.5	.	.
87	Hazel	Check	414.6	888.6	470.2	52.0	155.9	90.7	.	.
88	Starter	Check	311.1	727.3	493.6	51.9	169.1	67.1	.	.
89	Starter	Check	348.0	765.1	492.1	53.8	172.8	67.7	.	.
90	Premier	Check	316.8	713.4	496.0	50.1	160.6	65.6	.	.
91	Premier	Check	345.2	779.0	516.6	51.2	155.1	66.7	.	.
92	Marion	Check	404.7	970.2	473.6	54.5	150.7	75.6	.	.
93	Marion	Check	444.3	1021.4	483.7	56.3	155.0	76.0	.	.
94	Noble	Check	325.0	740.4	484.8	41.9	179.2	63.0	.	.
95	Noble	Check	317.2	717.5	503.0	47.7	173.9	65.7	.	.
96	Ogle	Check	368.4	790.3	484.6	38.1	148.4	68.1	.	.
97	Ogle	Check	364.8	780.3	475.0	39.3	149.1	68.2	.	.
98	Don	Check	338.5	737.9	473.9	44.7	149.1	75.2	.	.
99	Don	Check	330.2	681.1	481.4	50.0	149.8	75.8	.	.
100	IAN979-5-2	Check	373.3	853.7	467.7	64.4	170.8	84.1	.	.
Mean [†]			325.2	758.7	482.0	48.5	161.7	71.9		
LSD [‡]	Entry vs Entry		161.3	345.5	31.0	6.3	12.9	3.8		

[†] Mean of all entries evaluated in 1997 at Nashua.

[‡] Least significant difference at the 0.05 probability level.

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